Appl. No. 09/943,664
Amdmt. dated Dec mber 24, 2003
Reply to Office Action of September 24, 2003

REMARKS

In the Specification:

Applicant thanks the Examiner for withdrawing the objections to the specification raised in the Office Action of March 24, 2003.

In the Claims:

Claims 25-32 have been amended to clarify that the claimed polypeptides are isolated from lung or colon tissue and are encoded by nucleic acids which are amplified in lung and/or colon tumors. No new matter is added by this amendment and support for amendment of claims 25-32 may be found at page 29 and at Example 28, pages 119-137 of the specification.

New claims 35-36 have been added. New claims 35-36 do not encompass new matter and are supported at pages 59-62 of the specification.

Claims 22-24 are canceled herein without prejudice or disclaimer.

Priority Determination:

The Examiner contends that the effective priority date for the present application is December 1, 1999, the filing date of PCT/US99/28301. Applicant respectfully disagrees. The present application has utility and is enabled for use as a diagnostic for a tumor in a tissue, which was disclosed in provisional application 60/113,296, filed December 22, 1998. Therefore the proper priority date for the present invention is December 22, 1998.

Specifically, as stated in the previous Response and Request for Reconsideration mailed June 24, 2003, 60/113,296 describes three specific uses for the claimed invention: (1) as part of ribozyme and/or triple helix sequences which, in turn may be used in regulation of amplified genes (page 3, lines 23-25); (2) for determining the

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presence of PRO347 (page 3, lines 26-32); and (3) for diagnosing a tumor by detecting the level of expression of a gene encoding PRO347 (page 3, lines 33-35 – page 4, lines 1-24). Further, at pages 23-28, 60/113,296 discusses detecting gene amplification/expression of PRO347 in certain tissues and at pages 28-29, 60/113,296 describes anti-PRO347 antibody binding studies, which may be used to detect the polypeptide of SEQ ID NO:50.

Moreover, at pages 55-101, 60/113,296 describes methods for determining whether the genes encoding various PRO polypeptides are amplified in the genome of certain human lung, colon and/or breast cancers and/or cell lines. As with U.S. Application Serial No. 09/944,896, the gene amplification examples measure and discuss Δ Ct values.

Table 2, found at pages 65-72 sets forth the Δ Ct values for various PRO polypeptides in various tissues. The Δ Ct values for PRO347 are listed in the 8th column from the top, left-hand side of the page. This data demonstrates that the PRO347 gene is amplified in cancerous tissues. The results of the gene amplification study with respect to PRO347 are discussed at page 105, lines 22-33. Amplification of PRO347 DNA was detected in various tumors and therefore, as stated at page 105, lines 32-33, "antagonists, (e.g. antibodies) directed against the protein encoded by DNA44176 (PRO347) would be expected to be useful in cancer therapy." Those of skill in the art would also recognize that the nucleic acid encoding the protein associated with cancer, as well as the protein itself would also have diagnostic utility.

The Examiner's priority determination is based on her finding that the claimed invention is not supported by either a specific and substantial or a well-established utility. Applicant addresses the Examiner's concerns regarding utility below under the heading 35 U.S.C. § 101 and § 112 and respectfully requests the Examiner also consider those arguments in determining priority.

Claim Rejections:

35 U.S.C. § 102(e)

The Examiner has rejected claims 22-27, 31, 33, and 34 under 35 U.S.C. § 102 (e) as being anticipated by Holtzman *et al.*, U.S. Patent Application Publication US20020028508, effective filing date, April 23, 1998. Specifically, the Examiner alleges that Holtzman *et al.* disclose a protein that is 96.8% identical to the protein of SEQ ID NO: 50, particularly amino acids 27-109 of SEQ ID NO:50.

Applicant respectfully disagrees that Holtzman *et al.* anticipates the claimed invention. First, "[t]o serve as an anticipating reference, the reference must enable that which it is asserted to anticipate. 'A claimed invention cannot be anticipated by a prior art reference if the allegedly anticipatory disclosure cited as prior art is not enabled.'" *See Elan Pharm., Inc. v. Mayo Found. For Med. Ed. and Research,* 2003 U.S. App. LEXIS 20195 (Fed. Cir. 2003) citing *Amgen, Inc. v. Hoechst Marion Roussel, Inc.,* 314 F.3d 1313, 1354 (Fed. Cir. 2003). Applicants submit that Holtzman *et al.* is not enabled because the nucleic acid, protein and antibody cited by the Examiner (hereinafter collectively referred to as "T139") are not supported by either a specific and substantial utility or a well-established utility.

Specifically, Holtzman *et al.* discloses both the nucleic and amino acid sequences of T139 and reference a deposit of a cDNA (ATCC 98694). As the Examiner notes, the nucleic acid sequence disclosed by Holtzman *et al.* is 94.1% identical to the nucleic acid molecule of SEQ ID NO:49 and the amino acid sequence disclosed by Holtzman *et al.* 96.8% identical to the protein of SEQ ID NO:50. Much like the present specification, Holtzman *et al.* discloses various characteristics of the cDNA sequence encoding T139, as well as various predicted characteristics of the T139 protein (p. 8, paragraph 0107). Also much like the present specification, Holtzman *et al.* discloses that sequence analysis revealed various homologies, for example T139 is described as homologous to testis-specific protein-1 (TPX-1) (page 8, paragraph 0110). Holtzman *et al.* also explains generally various variant T139 sequences, antibodies to T139, assays, and methods of treatment. In addition, Holtzman *et al.* discloses the isolation and

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characterization of T139 cDNA, the distribution of T139 mRNA in human tissues and the predicted characterization and production of T139 proteins. However, unlike the present specification, Holtzman *et al.* does not enable one of skill in the art to use T139. Specifically, although Holtzman *et al.* generally notes that T139 might be used to modulate the function, morphology, proliferation and/or differentiation of cells in tissues in which it is expressed (p. 39, paragraph 0367), or used to treat renal (kidney) disorders (p.39-40, paragraph 0375), or used to treat testicular disorders (p. 40, paragraph 0376), Holtzman *et al.* does not disclose any working example of a credible, specific and substantial utility for T139. Hence, Applicant submits that Holtzman *et al.* does not enable that which it is asserted to anticipate and therefore, does not anticipate the present invention.

In addition, as stated above, Applicant has canceled claims 22-24 without prejudice or disclaimer and has amended claims 25-32 to clarify that the claimed polypeptides are isolated from lung or colon tissue and are encoded by a nucleic acid that is amplified in lung and/or colon tumors. "A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." *Verdegaal Bros. v. Union Oil Co. of California*, 814 F.2d 628, 631, 2 USPQ2d 1051, 1053 (Fed. Cir. 1987). MPEP § 2131.01. Holtzman *et al.* neither explicitly nor inherently discloses polypeptides isolated from lung or colon tissue, which are encoded by a nucleic acid that is amplified in lung and/or colon tumors and therefore, cannot anticipate these claims.

Holtzman *et al.* does teach that the protein cited by the Examiner, T139 (hereafter "T139"), is homologous to testis-specific protein (see p. 8, paragraph 0110) and plays a role in kidney defects such as kidney failure or hyperplasia (see p. 38, paragraph 0359). However, Holtzman *et al.* does not disclose or examine the presence of T139 protein or nucleic acid in lung or colon tumor tissue. Instead, at page 41, paragraph 0397, Holtzman *et al.* discloses that mRNA encoding the protein cited by the Examiner is expressed at high levels in the kidney with lower levels in the testis but that "[n]o other tissue examined (heart, brain, placenta, **lung**, liver, skeletal muscle, pancreas, spleen,

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thymus, ovaries, small intestine, **colon** and peripheral blood leukocytes) showed any expression." (emphasis added). *See also* p. 8, paragraph 0113. Thus, Holtzman *et al.* does not anticipate the present claims, which are directed to polypeptides isolated from lung and colon tissues that are encoded by a nucleic acid which is amplified in lung and colon tumors. Hence, Applicant has overcome this ground of rejection for claims 25-27, 31, 33, and 34 and respectfully requests that it be withdrawn.

35 U.S.C. § 112, Second Paragraph

Claims 22-27, 31, 33, and 34 are rejected under 35 U.S.C. § 112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention. Specifically, the Examiner contends that the recitation of "the extracellular domain" . . . lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell.

Applicant respectfully disagrees that the claims are indefinite. As taught by the Alberts *et al.* textbook, Molecular Biology of the Cell, 3rd edition, (pp. 557-560; Appendix A), a signal sequence is not *necessarily* cleaved from the extracellular domain of a protein, even though a "signal peptide is often (but not always) removed from the finished protein...." *Id.* For example, in polypeptides with both signal sequences and distant transmembrane domains, the polypeptide can exist as a transmembrane polypeptide with its signal sequence uncleaved. The signal sequence is later cleaved with the transmembrane domain influencing the cleavage process. *See e.g.,* Rehm et al., EMBO J. 7:1573-1582 (April 2, 2001) (Appendix A). Depending on further processing, the polypeptide can either later be released as a soluble polypeptide or remain a transmembrane polypeptide. Thus, Applicant respectfully submits that the art *does* recognize that a signal sequence can be part of an extracellular domain.

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Applicant has canceled claims 22-24 without prejudice or disclaimer. Accordingly, Applicant respectfully requests that the rejections of claims 25-27, 30-31, 33-34 under 35 U.S.C. § 112 ¶2 for indefiniteness be withdrawn.

35 U.S.C. § 101 and § 112

Claims 22-34 remain rejected under 35 U.S.C. § 101 because the Examiner maintains that the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility. Applicant notes that the Examiner bases her rejection on her careful consideration of the Goddard Declaration. Specifically, the Examiner states that the declaration addresses her concerns regarding the significance of a difference of 1 or 2 PCR cycles, as well as her concerns regarding whether proper controls for aneuploidy were used, and therefore, the Examiner concludes that the nucleic acid molecule of SEQ ID NO:49 would have utility, and would be enabled as being useful as a probe to diagnose certain cancers. However, the Examiner notes that the claims of the present application are directed to polypeptides. The Examiner, citing Pennica *et al.,* asserts that it does not necessarily follow that an increase in gene copy number results in increased gene and protein expression. The Examiner also argues citing Haynes *et al.* that an increase in mRNA expression does not necessarily result in increased protein expression.

Applicant respectfully disagrees that the present claims are not supported by either a specific and substantial utility or a well-established utility. The pending claims are directed to polypeptides encoded by an amplified DNA sequence. The specification specifically asserts a utility for these polypeptides. See, for example, page 137, lines 24-25, stating that "polypeptides encoded by the (amplified) DNAs tested have utility as diagnostic markers for determining the presence of tumor cells in lung and/or colon tissue samples." An Applicant's assertion of utility creates a presumption of utility that will be sufficient to satisfy the utility requirement of 35 U.S.C. § 101, "unless there is a reason for one skilled in the art to question the objective truth of the statement of utility or its scope." *In re Langer,* 503 F.2d 1380, 1391, 183 USPQ 288, 297 (CCPA 1974). *See also In re Jolles,* 638 F.2d 1322, 206 USPQ 885 (CCPA 1980); *In re Irons,* 340

F.2d 974, 144 USPQ 351 (9165); *In re Sichert*, 566 F.2d 1154, 1159, 196 USPQ 209, 212-213 (CCPA 1977).

Moreover, in order to satisfy the utility requirement of 35 U.S.C. § 101, Applicant need only provide one credible assertion of specific and substantial utility **or well-established utility** for each claimed invention. The credibility of the asserted utility is to be assessed from the perspective of one of ordinary skill in the art in view of the disclosure and any other evidence of record (e.g., test data, affidavits or declarations from experts in the art, patents or printed publications) that is probative of Applicant's assertions. MPEP § 2107-II(B)(ii) (8th ed. 2001).

Compliance with 35 U.S.C. § 101 is a question of fact. *Raytheon v. Roper*, 724 F.2d 951, 956, 220 USPQ 592, 596 (Fed. Cir. 1983) *cert. denied*, 469 U.S. 835 (1984). The evidentiary standard to be used throughout *ex parte* examination in setting forth a rejection is a preponderance of the totality of the evidence under consideration. *In re Oetiker*, 977 F.2d 1443, 1445, 24 USPQ2d 1443, 1444 (Fed. Cir. 1992). Thus, to overcome the presumption of truth that an assertion of utility by the Applicant enjoys, the Examiner must establish that it is more likely than not that one of ordinary skill in the art would doubt the truth of the statement of utility. Only after the Examiner makes a proper *prima facie* showing of lack of utility, does the burden of rebuttal shift to the Applicant. The issue will then be decided on the totality of the evidence.

In the present case a *prima facie* case of lack of utility has not been established. First, one basis for the Examiner's conclusion of lack of utility is based on a quote from Pennica *et al*, cited in the Goddard Declaration, which was filed with and discussed in Applicant's Amendment and Request for Reconsideration mailed June 24, 2003. Based on this reference, the Examiner correctly concludes that increased copy number does not *necessarily* result in increased protein expression. The standard, however, is not absolute certainty. The fact that in the case of a specific class of closely related molecules there seemed to be no correlation between gene amplification and the level of mRNA/protein expression, does not establish that it is more likely than not, in

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general, that such correlation does not exist. The Examiner has not shown whether the lack of correlation observed for the family of polypeptides referenced in Pennica *et al.* is typical, or is merely a discrepancy, an exception to the rule of correlation.

Moreover, the totality of the evidence demonstrates that the present claims are supported by a specific and substantial utility. Specifically, even if one assumes *arguendo* that it is more likely than not that there is no correlation between gene amplification and increased mRNA/protein expression, a polypeptide encoded by a gene that is amplified in cancer would still have a specific and substantial utility. Enclosed herein is a declaration of Avi Ashkenazi, Ph.D., an expert in the biology of cancer and an inventor of the present invention. As Dr. Ashkenazi explains at paragraph 6 of his declaration:

> [E]ven when amplification of a cancer marker gene does not result in significant over-expression of the corresponding gene product, this very absence of gene product over-expression of the corresponding gene product still provides significant information for cancer diagnosis and treatment. Thus, if over-expression of the gene product does not parallel gene amplification in certain tumor types but does so in others, then parallel monitoring of gene amplification and gene product over-expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over-expression is crucial information for the practicing clinician. If a gene is amplified but the corresponding gene product is not over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

Accordingly, the PRO347 polypeptide has a substantial, specific utility, and Applicant respectfully requests that the Examiner withdraw the present rejection.

In view of these remarks, Applicant respectfully submits that the claimed invention has utility and is fully enabled. Accordingly, Applicant respectfully requests that the Examiner reconsider and withdraw the rejection of claims 25-34 under 35 U.S.C. § 101.

35 U.S.C. § 112, first paragraph

Claims 22-34 remain rejected under 35 U.S.C. § 112, first paragraph, for lack of enablement based on the Examiner's maintaining her position that the claimed invention

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is not supported by either a specific and substantial asserted utility or a well established utility. Applicant submits that as explained above, Claims 25-34 are supported by both a specific and substantial utility and a well-established utility. Therefore, this ground of rejection has been overcome and Applicant respectfully requests that it be withdrawn.

Enablement

The Examiner has further rejected Claims 22-34 under 35 U.S.C. 112, first paragraph, alleging that even if the specification were enabling of how to use the PRO347 polypeptide, enablement would not be found commensurate in scope with the claims. Specifically, the Examiner contends that the specification does not enable one of skill in the art to use fragments or variants of PRO347 because although the data in the specification shows that gene copy number is increased in certain tumor tissue samples, it is not predictable that the PRO347 polypeptide is overexpressed in any tumor cell in which the encoding nucleic acid is amplified.

Applicant respectfully disagrees. MPEP §2164.03 states that "'[t]he predictability or lack thereof' in the art refers to the ability of one skilled in the art to extrapolate the disclosed or known results to the claimed invention. If one skilled in the art can readily anticipate the effect of a change within the subject matter to which the claimed invention pertains, then there is predictability in the art." Applicant submits that utility of the claimed polypeptide is predictable to one of skill in the art. Further, Applicant discloses in the specification at page 119, lines 27-30, that in the art, the general presumption is that gene amplification is associated with overexpression of the gene product. Thus, it is predictable that a nucleic acid encoding a gene that is amplified in tumor tissues would also encode a polypeptide that is overexpressed in tumor tissues and therefore, one of skill in the art would know that such polypeptides would have utility as diagnostic markers for determining the presence of tumor cells in lung and/or colon tissue samples.

In addition, one of skill in the art would know that the claimed polypeptides would have significant utility even in the absence of overexpression of gene product. As discussed

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above, Dr. Ashkenazi explains in paragraph five of his declaration that "[e]ven in the absence of over-expression of the gene product, amplification of a cancer marker gene is useful in the diagnosis or classification of cancer, or in predicting or monitoring the efficacy of cancer therapy."

Dr. Ashkenazi further explains the relationship between the gene amplification data presented in the specification and gene product (protein) expression in paragraph six stating:

> the very absence of gene product over expression . . . provides significant information . . . . (For example,) . . . if over-expression of the gene product does not parallel gene amplification in certain tumor types but does so in others, then parallel monitoring of gene amplification and gene product over-expression enables more accurate tumor classification and hence better determination of suitable therapy.

Dr. Ashkenazi also points out that absence of over-expression of gene product is "crucial information" for the practicing clinician when determining which agents to use in treating a patient. For example, in such a situation agents that target gene product would not be effective. Hence, Applicant submits that one of skill in the art is enabled to practice the claimed invention and respectfully requests that the rejection of claims 25-34 be withdrawn.

Written Description

Claims 22-26, 33, and 34 remain rejected under 35 U.S.C. 112, first paragraph as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Specifically, the Examiner contends that amplification of a nucleic acid does not necessarily result in an increase of the encoded polypeptide, and therefore the functional recitation is not considered adequate to overcome the written description requirement.

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Applicant respectfully disagrees and submits that Claims 22-26, 33, and 34 are adequately described in the present application. First, as mentioned above, Applicant has clarified that the claimed nucleic acid is amplified in lung and/or colon tumors. Second, as the Examiner notes, the written description requirement requires that an applicant's specification convey with reasonable clarity to those skilled in the art, that as of the filing date sought, he or she was in possession of the invention. *Vas-Cath, Inc. v. Mahurkar,* 19 USPQ2d 1111, 1116 (Fed. Cir. 1991). Moreover, in order to have possession of members of a claimed genus, the specification **need not** describe all of the species that the genus encompasses. *Amgen Inc. v. Chugai Pharmaceutical Co.,* 18 USPQ2d 1016, 1027 (Fed. Cir. 1991). Applicant has demonstrated possession of the claimed invention, at least by disclosure of SEQ ID NOS: 49 and 50, as well as by deposit of DNA44176-1244 on December 10, 1997 as disclosed on page 148 of the specification (ATCC deposit no. ATCC209532).

Further, compliance with the written description requirement does not require an applicant to describe exactly the subject matter claimed; rather, the description must clearly allow a person of ordinary skill in the art to recognize that he or she invented what is claimed. *Vas-Cath Inc. v. Mahurkar,* 19 USPQ2d 1111, 1116 (Fed. Cir. 1991). The analysis for determining whether the present specification provides written description support for the invention defined by claims 22-26, 33 and 34 may be performed by numerous methods, several of which are described in the Guidelines and further exemplified in the Revised Interim Written Description Guidelines Training Materials ("Written Description Training Materials"), published on the USPTO website at http://www.uspto.gov/web/offices/pac/writtendesc.pdf. These Written Description Training Materials are designed to provide additional clarity to the Guidelines which are published in the Federal Register, Volume 66, No. 4, pages 1099-1111. In fact, as indicated in the USPTO press release of March 1, 2000 introducing the Written Description Examination Training Materials (Press Release #00-15), these training materials were promulgated by the USPTO and are:

> "designed to <u>aid PTO's patent examiners in applying the interim written description and utility guidelines in a uniform and consistent manner</u> to promote

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the issuance of high quality patents. The training materials will also <u>assist patent applicants in responding to the PTO</u> when utility or written description issues are raised during the examination of a patent application." (emphasis added)

With regard to claims 25-26, 33, and 34, the present situation is analogous to Example 14 on pages 53-55 of the Written Description Training Materials. More specifically, in Example 14 on pages 53-55 of the enclosed Written Description Training Materials, a claim directed to a protein and variants thereof having 95% sequence identity, all of which share the same biological function, is analyzed for its compliance with the written description requirement of 35 U.S.C. § 112, first paragraph. The Written Description Training Materials conclude that such a claim satisfies the written description requirement of 35 U.S.C. § 112, first paragraph, when (1) a single protein sequence is actually reduced to practice, (2) procedures for making variants of that "reduced to practice" protein sequence are conventional in the art, and (3) an assay is described which allows identification of other proteins having the same biological activity. The reasoning provided by the USPTO in the Written Description Training Materials is that:

"[t]here is actual reduction to practice of the single disclosed species. The specification indicates that <u>the genus of proteins that must be variants of SEQ ID NO:...</u>does not have substantial variation<u> since all of the variants must possess the specified [biological function] and must have at least 95% identity to the reference sequence</u>, SEQ ID NO:...<u>The single species disclosed *is representative of the genus*</u> because all members have at least 95% structural identity with the reference compound and because of the presence of an assay which applicant provided for identifying all of the at least 95% identical variants of SEQ ID NO:...which are capable of the specified [biological function]. <u>One of skill in the art would conclude that applicant was in possession of the necessary common attributes possessed by members of the genus.....{As such], the disclosure meets the requirements of 35 U.S.C. § 112, first paragraph, as providing adequate written description for the claimed invention.</u>" (emphasis added).

Analogous to Example 14 of the Written Description Training Materials, the present specification discloses and actually reduces to practice a polypeptide recited in claims 25-26, 33 and 34 (*i.e.*, SEQ ID NO:50) as well as a nucleic acid encoding that polypeptide (*i.e.*, SEQ ID NO:49). Moreover, the polypeptide variants encompassed within claims 25-26, 33, and 34 ***do not have substantial variation*** with SEQ ID NO:50 because (a) they share at least 95% sequence identity with SEQ ID NO:50 or the encoding nucleic acid (SEQ ID NO:49) (Applicants note that methods for routinely determining nucleic acid and/or amino acid sequence identity are described in detail in the present specification at page 23, line 34 to page 29, line 2, *see also* pages 34-54), and (b) they share the biological function of being encoded by a nucleic acid that is amplified in lung and/or colon tumors. (Applicants note that the specification describes in detail in Example 28 an assay that is useful for identifying nucleic acids encoding polypeptides having this biological function). As such, the polypeptides encompassed within claims 25-26, 33, and 34 all share substantial common structural features (*i.e.*, at least 80% sequence identity) and substantial common functional features (*i.e.,* being encoded by a nucleic acid that is amplified in lung and/or colon tumors). Moreover, the present specification also describes conventionally known methods used and known in the art for preparing a multitude of variants (see the present specification at page 59, line 13 to page 63, line 36).

In view of the legal standard regarding the written description requirement under 35 U.S.C. § 112, first paragraph, in combination with the interpretation of the written description requirement by the United States Patent and Trademark Office as set forth in the Guidelines, and given the above, Applicants respectfully submit that currently pending claims 25-26, 33 and 34 satisfy the written description requirement of 35 U.S.C. § 112, first paragraph because it would be clear to one of skill in the art that Applicant possessed the claimed subject matter at the time of filing the instant application.

Moreover, claims 25-26 are analogous to the claim found to satisfy the written description requirement in Example 14 of the enclosed Written Description Training Materials. As such, under the Guidelines and the examination training materials

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promulgated by the USPTO for ensuring consistent examination of written description compliance during prosecution of patent applications, the written description requirement of 35 U.S.C. § 112, first paragraph, is satisfied for claims 25-26, 33 and 34. Therefore, Applicant respectfully requests this ground of rejection be withdrawn.

35 U.S.C. § 102(a)

Claims 22-34 are rejected under 35 U.S.C. 102(a) as being anticipated by Botstein *et al.*, WO 99/35170, published July 15, 1999. Applicant has demonstrated that the proper priority date of the instant application is December 22, 1998, before Botstein *et al* was published. Therefore, this ground of rejection has been overcome and Applicant respectfully requests that it be withdrawn.

Claims 22-27, 31, 33, and 34 are further rejected under 35 U.S.C. 102(a) as being anticipated by Holtzman, WO 99/54343, published October 28, 1999. As discussed above, Applicant has demonstrated that the proper priority date of the instant application is December 22, 1998, also before Holtzman was published. Therefore, this ground of rejection has also been overcome and Applicant respectfully requests that it be withdrawn.

SUMMARY

Applicant believes that currently pending Claims 25-36 are patentable. Applicant respectfully requests the Examiner grant early allowance of this application. The Examiner is invited to contact the undersigned attorneys for the Applicant via telephone if such communication would expedite this application.

Respectfully submitted,

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MOLECULAR BIOLOGY OF
THE CELL
THIRD EDITION

Bruce Alberts • Dennis Bray
Julian Lewis • Martin Raff • Keith Roberts
James D. Watson

Bruce Alberts received his Ph.D. from Harvard University and is currently President of the National Academy of Sciences and Professor of Biochemistry and Biophysics at the University of California, San Francisco. *Dennis Bray* received his Ph.D. from the Massachusetts Institute of Technology and is currently a Medical Research Council Fellow in the Department of Zoology, University of Cambridge. *Julian Lewis* received his D.Phil. from the University of Oxford and is currently a Senior Scientist in the Imperial Cancer Research Fund Developmental Biology Unit, University of Oxford. *Martin Raff* received his M.D. from McGill University and is currently a Professor in the MRC Laboratory for Molecular Cell Biology and the Biology Department, University College London. *Keith Roberts* received his Ph.D. from the University of Cambridge and is currently Head of the Department of Cell Biology, the John Innes Institute, Norwich. *James D. Watson* received his Ph.D. from Indiana University and is currently Director of the Cold Spring Harbor Laboratory. He is the author of *Molecular Biology of the Gene* and, with Francis Crick and Maurice Wilkins, won the Nobel Prize in Medicine and Physiology in 1962.

Front cover: The photograph shows a rat nerve cell in culture. It is labeled (*yellow*) with a fluorescent antibody that stains its cell body and dendritic processes. Nerve terminals (*green*) from other neurons (not visible), which have made synapses on the cell, are labeled with a different antibody. (Courtesy of Olaf Mundigl and Pietro de Camilli.)

Dedication page: Gavin Borden, late president of Garland Publishing, weathered in during his mid-1980s climb near Mount McKinley with MBoC author Bruce Alberts and famous mountaineer guide Mugs Stump (1940–1992).

Back cover: The authors, in alphabetical order, crossing Abbey Road in London on their way to lunch. Much of this third edition was written in a house just around the corner. (Photograph by Richard Olivier.)

Figure 12–5 Hypotheses for the evolutionary origins of some membrane-bounded organelles. The origins of mitochondria, chloroplasts, ER, and the cell nucleus could explain the topological relationships of these intracellular compartments in eucaryotic cells. (A) A possi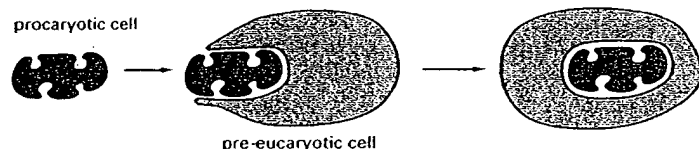ble pathway for the evolution of the cell nucleus and the ER. In some bacteria the single DNA molecule is attached to an invagination of the plasma membrane, called a *mesosome*. Such an invagination in a very ancient procaryotic cell could have spread to form an envelope around the DNA while still allowing access of the DNA to the cell cytosol (as is required for DNA to direct protein synthesis). This envelope is presumed to have eventually pinched off completely from the plasma membrane, producing a nuclear compartment surrounded by a double membrane. As illustrated, the nuclear envelope is organized by a fibrous shell called the *nuclear lamina* and is penetrated by communicating channels called *nuclear pore complexes*. Because it is surrounded by two membranes that are in continuity where they are penetrated by these pores, the nuclear compartment is topologically equivalent to the cytosol. The lumen of the ER is continuous with the space between the inner and outer nuclear membranes and topologically equivalent to the extracellular space. (B) Mitochondria (and chloroplasts) are thought to have originated when a bacterium was engulfed by a larger pre-eucaryotic cell. They retain their autonomy. This may explain why the lumens of these organelles remain isolated from the vesicular traffic that interconnects the lumens of many other intracellular compartments.

plasma membrane of the bacterium, while the lumen of these organelles evolved from the bacterial cytosol. As might be expected from such origins, these two organelles remain isolated from the extensive vesicular traffic that connects the interiors of most of the other membrane-bounded organelles to one another and to the outside of the cell.

This evolutionary scheme groups the intracellular compartments in eucaryotic cells into five distinct families: (1) the nucleus and the cytosol, which communicate through the nuclear pores and are thus topologically continuous (although functionally distinct); (2) all organelles that function in the secretory and endocytic pathways—including the ER, Golgi apparatus, endosomes, lysosomes, and numerous classes of transport vesicles; (3) the mitochondria; (4) the plastids (in plants only); and (5) the peroxisomes (whose evolutionary origins are discussed later).

Proteins Can Move Between Compartments in Different Ways [3]

All proteins begin being synthesized on ribosomes in the cytosol, except for the few that are synthesized on the ribosomes of mitochondria and plastids. Their subsequent fate depends on their amino acid sequence, which can contain **sorting signals** that direct their delivery to locations outside the cytosol. Most proteins do not have a sorting signal and consequently remain in the cytosol as permanent residents. Many others, however, have specific sorting signals that direct their transport from the cytosol into the nucleus, the ER, mitochondria, plastids (in plants), or peroxisomes; sorting signals can also direct the transport of proteins from the ER to other destinations in the cell.

To understand the general principles by which sorting signals operate, it is important to distinguish three fundamentally different ways by which proteins move from one compartment to another. (1) The protein traffic between the cytosol and nucleus occurs between topologically equivalent spaces, which are in continuity through the nuclear pore complexes. This process is called **gated transport** because the nuclear pore complexes function as selective gates that can actively transport specific macromolecules and macromolecular assemblies, although they also allow free diffusion of smaller molecules. (2) In **transmembrane transport** membrane-bound *protein translocators* directly transport specific proteins across a membrane from the cytosol into a space that is topologically distinct. The transported protein molecule usually must unfold in order to snake

Figure 12-6 The "sidedness" of membranes is preserved during vesicular transport. Note that the original orientation of both proteins and lipids in the donor-compartment membrane is preserved in the target-compartment membrane and that soluble molecules are transferred from lumen to lumen.

through the membrane. The initial transport of selected proteins from the cytosol into the ER lumen or into mitochondria, for example, occurs in this way. (3) In vesicular transport, transport vesicles ferry proteins from one compartment to another. The vesicles become loaded with a cargo of molecules derived from the lumen of one compartment as they pinch off from its membrane; they discharge their cargo into a second compartment by fusing with its membrane. The transfer of soluble proteins from the ER to the Golgi apparatus, for example, occurs in this way. Because the transported proteins do not cross a membrane, they move only between compartments that are topologically equivalent (Figure 12-6). We discuss vesicular transport in more detail in Chapter 13. The three ways in which proteins are transported between different compartments are summarized in Figure 12-7.

Each of the three modes of protein transfer is usually selectively guided by sorting signals in the transported protein that are recognized by complementary receptor proteins in the target organelle. If a large protein is to be imported into the nucleus, for example, it must possess a sorting signal that is recognized by receptor proteins associated with the nuclear pore complex. If a protein is to be transferred directly across a membrane, it must possess a sorting signal that is recognized by the translocator in the membrane to be crossed. Likewise, if a protein is to be incorporated into certain types of transport vesicles or to be retained in certain organelles, its sorting signal must be recognized by a complementary receptor in the appropriate membrane.
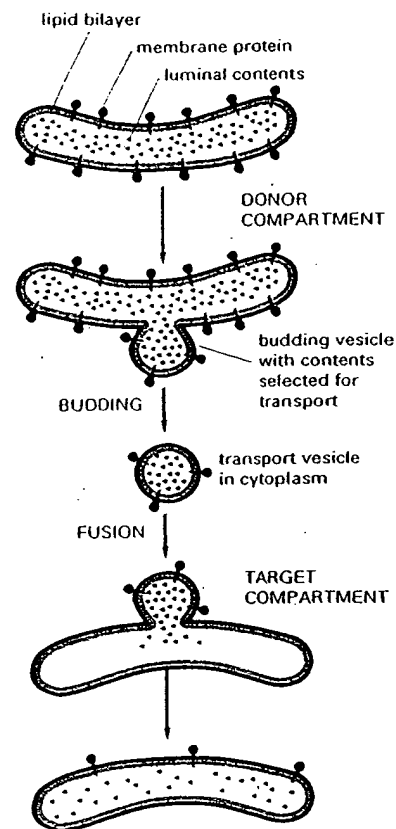
Signal Peptides and Signal Patches Direct Proteins to the Correct Cellular Address [4]

There are at least two types of sorting signals on proteins. One type resides in a continuous stretch of amino acid sequence, typically 15 to 60 residues long. This signal peptide is often (but not always) removed from the finished protein by a specialized signal peptidase once the sorting process has been completed. The other type consists of a specific three-dimensional arrangement of atoms on the

Figure 12-7 A simplified "road map" of protein traffic. Proteins can move from one compartment to another by gated transport (red), transmembrane transport (blue), or vesicular transport (green). The signals that direct a given protein's movement through the system, and thereby determine its eventual location in the cell, are contained in its amino acid sequence. The journey begins with the synthesis of a protein on a ribosome and terminates when the final destination is reached. At each intermediate station (boxes) a decision is made as to whether the protein is to be retained or transported further. In principle, a signal could be required either for retention in or for exit from each of the compartments shown, with the alternative fate being the default pathway (one that requires no signal). The vesicular transport of proteins from the ER through the Golgi apparatus to the cell surface, for example, appears not to require any specific sorting signals; specific sorting signals therefore are required to retain in the ER and the Golgi apparatus those specialized proteins that are resident there.

We shall use this figure repeatedly as a guide throughout this chapter and the next, highlighting the particular pathway being discussed.

UNFOLDED PROTEIN   FOLDED PROTEIN

(A)

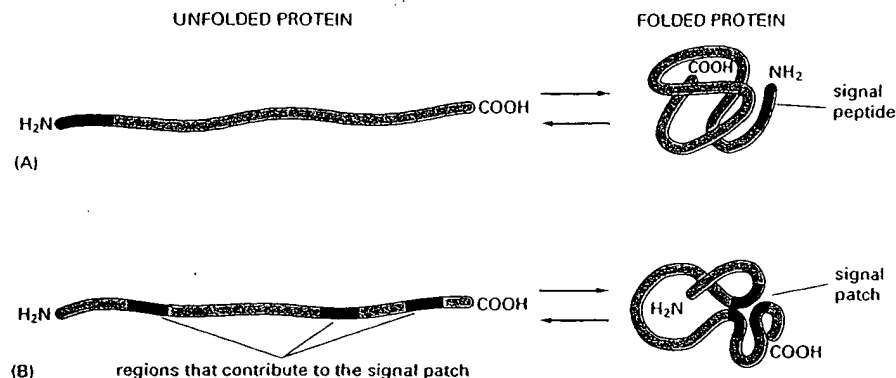(B)   regions that contribute to the signal patch
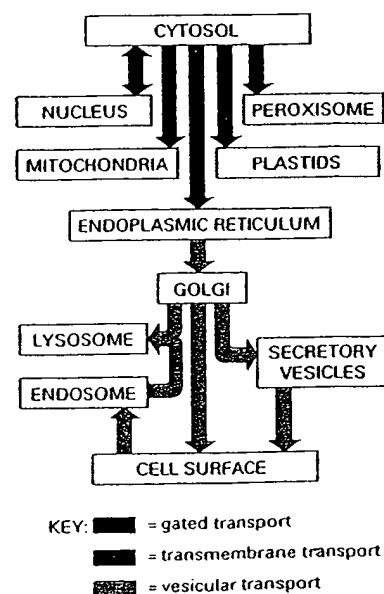
Figure 12-8 Two ways that a sorting signal can be built into a protein. (A) The signal resides in a single discrete stretch of amino acid sequence, called a *signal peptide*, that is exposed in the folded protein. Signal peptides often occur at the end of the polypeptide chain (as shown), but they can also be located elsewhere. (B) A *signal patch* can be formed by the juxtaposition of amino acids from regions that are physically separated before the protein folds (as shown); alternatively, separate patches on the surface of the folded protein that are spaced a fixed distance apart could form the signal. In either case the transport signal depends on the three-dimensional conformation of the protein, which makes it difficult to locate the signal precisely.

protein's surface that forms when the protein folds up. The amino acid residues that comprise this **signal patch** can be distant from one another in the linear amino acid sequence, and they generally remain in the finished protein (Figure 12-8). Signal peptides are used to direct proteins from the cytosol into the ER, mitochondria, chloroplasts, peroxisomes, and nucleus, and they are also used to retain soluble proteins in the ER. Signal patches identify certain enzymes that are to be marked with specific sugar residues that then direct them from the Golgi apparatus into lysosomes; signal patches are also used in other sorting steps that have been less well characterized.

Different types of signal peptides are used to specify different destinations in the cell. Proteins destined for initial transfer to the ER usually have a signal peptide at their amino terminus, which characteristically includes a sequence composed of about 5 to 10 hydrophobic amino acids. Most of these proteins will in turn pass from the ER to the Golgi apparatus, but those with a specific sequence of four amino acids at their carboxyl terminus are retained as permanent ER residents. Proteins destined for mitochondria have signal peptides of yet another type, in which positively charged amino acids alternate with hydrophobic ones. Proteins destined for peroxisomes usually have a specific signal sequence of three amino acids at their carboxyl terminus. Many proteins destined for the nucleus carry a signal peptide formed from a cluster of positively charged amino

Table 12-3 Some Typical Signal Peptides

Function of Signal Peptide	Example of Signal Peptide
Import into ER	⁺H₃N-Met-Met-Ser-Phe-Val-Ser- Leu-Leu-Leu-Val Gly-Ile-Leu-Phe-Trp-Ala -Thr-Glu-Ala-Glu- Gln-Leu-Thr-Lys-Cys-Glu-Val-Phe-Gln-
Retain in lumen of ER	-Lys-Asp-Glu-Leu-COO⁻
Import into mitochondria	⁺H₃N-Met-Leu-Ser-Leu-Arg-Gln-Ser-Ile-Arg-Phe- Phe-Lys-Pro-Ala-Thr-Arg-Thr-Leu-Cys-Ser- Ser-Arg-Tyr-Leu-Leu-
Import into nucleus	-Pro-Pro-Lys-Lys-Arg-Lys-Val-
Import into peroxisomes	-Ser-Lys-Leu-
Attach to membranes via the covalent linkage of a myristic acid to the amino terminus	⁺H₃N-Gly-Ser-Ser-Lys-Ser-Lys-Pro-Lys-

Positively charged amino acids are shown in *red* and negatively charged amino acids in *green*. An extended block of hydrophobic amino acids is enclosed in a *yellow* box. H₃N⁺ indicates the amino terminus of a protein; COO⁻ indicates the carboxyl terminus.

A transfection approach for defining signal sequences

One way to show that a signal sequence is required and sufficient to target a protein to a specific intracellular compartment is to create a fusion protein in which the signal sequence is attached by genetic engineering techniques to a protein that is normally resident in the cytosol. After the cDNA encoding this protein is transfected into cells, the location of the fusion protein is determined by immunostaining or by cell fractionation.

signal sequence a or b   gene encoding cytosolic protein

plasmid used to transfect cells

signal sequence a (▨) directs fusion protein to organelle A

signal sequence b (■) directs fusion protein to organelle B
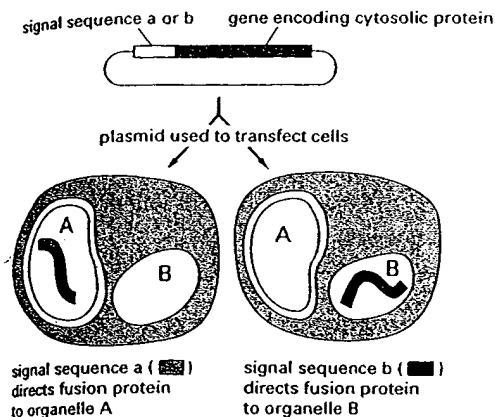
· By altering the signal sequence using site-directed mutagenesis, one can determine which structural features are important for its function.

A biochemical approach for studying the mechanism of protein translocation
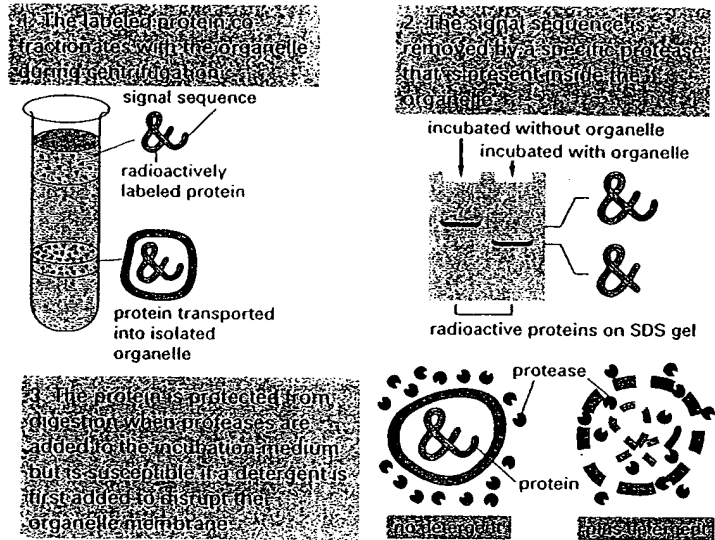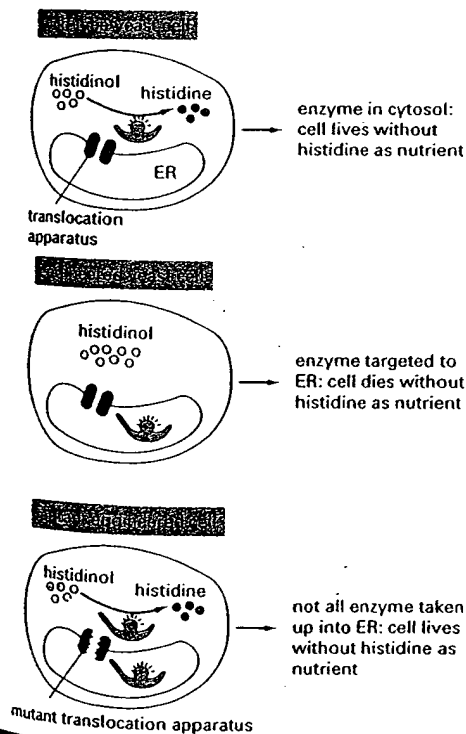
In this approach a labeled protein containing a specific signal sequence is transported into isolated organelles in vitro. The labeled protein is usually produced by cell-free translation of a purified mRNA encoding the protein; radioactive amino acids are used to label the newly synthesized protein so that it can be distinguished from the many other proteins that are present in the in vitro translation system.

Three methods are commonly used to test if the labeled protein has been translocated into the organelle:

1. The labeled protein co-fractionates with the organelle during centrifugation

signal sequence

radioactively labeled protein

protein transported into isolated organelle

2. The signal sequence is removed by a specific protease that is present inside the organelle

incubated without organelle

incubated with organelle

radioactive proteins on SDS gel

3. The protein is protected from digestion when proteases are added to the incubation medium but is susceptible if a detergent is first added to disrupt the organelle membrane

protease

protein

undigested

digested

By exploiting such in vitro assays, one can determine what components (proteins, ATP, GTP, etc.) are required for the translocation process.

Genetic approaches for studying the mechanism of protein translocation

histidinol   histidine

ER

translocation apparatus

enzyme in cytosol: cell lives without histidine as nutrient

histidinol

enzyme targeted to ER: cell dies without histidine as nutrient

histidinol   histidine

mutant translocation apparatus

not all enzyme taken up into ER: cell lives without histidine as nutrient

Yeast cells with mutations in genes that encode components of the translocation machinery have been useful for studying protein translocation. Because mutant cells that cannot translocate proteins across their membranes will die, the trick is to design a strategy that allows weak mutations that cause only a partial defect in protein translocation to be isolated.

One way uses genetic engineering to design special yeast cells. The enzyme histidinol dehydrogenase, for example, normally resides in the cytosol, where it is required to produce the essential amino acid histidine from its precursor histidinol. A yeast strain is constructed in which the histidinol dehydrogenase gene is replaced by a re-engineered gene encoding a fusion protein with an added signal sequence that misdirects the enzyme into the endoplasmic reticulum (ER). When such cells are grown without histidine, they die because all of the histidinol dehydrogenase is sequestered in the ER, where it is of no use. Cells with a mutation that partially inactivates the mechanism for translocating proteins from the cytosol to the ER, however, will survive because enough of the dehydrogenase will be retained in the cytosol to produce histidine. Often one obtains a cell in which the mutant protein still functions partially at normal temperature but is completely inactive at higher temperature. A cell carrying such a temperature-sensitive mutation dies at higher temperature, whether or not histidine is present, as it cannot transport any protein into the ER. This allows the normal gene that was disabled by the mutation to be identified by transfecting the mutant cells with a yeast plasmid vector into which random yeast genomic DNA fragments have been cloned: the specific DNA fragment that rescues the mutant cells when they are grown at high temperature should encode the wild-type version of the mutant gene.

acids, which is commonly found at internal sites of the polypeptide chain. Some typical signal peptides are listed in Table 12-3.

The importance of each of these signal peptides for protein targeting has been shown by experiments in which the peptide is transferred from one protein to another by genetic engineering techniques: placing the amino-terminal ER signal peptide at the beginning of a cytosolic protein, for example, redirects the protein to the ER. Even though their amino acid sequences can vary greatly, the signal peptides of all proteins having the same destination are functionally interchangeable: physical properties, such as hydrophobicity, often appear to be more important in the signal-recognition process than the exact amino acid sequence.

Signal patches are far more difficult to analyze than signal peptides, and so less is known about their structure. Because they result from a complex three-dimensional protein-folding pattern, they cannot be easily transferred experimentally from one protein to another.

The main ways of studying how proteins are directed from the cytosol to a specific compartment and how they are translocated across membranes are illustrated in Panel 12-1 (p. 559).

Cells Cannot Construct Their Membrane-bounded Organelles *de Novo:* They Require Information in the Organelle Itself [5]

When a cell reproduces by division, it has to duplicate its membrane-bounded organelles. In general, cells do this by enlarging the existing organelles by incorporating new molecules into them; the enlarged organelles then divide and are distributed to the two daughter cells. Thus each daughter cell inherits from its mother a complete set of specialized cell membranes. This inheritance is essential because a cell could not make such membranes *de novo.* If the ER were completely removed from a cell, for example, how could the cell reconstruct it? The membrane proteins that define the ER and carry out many of its functions are themselves products of the ER. A new ER could not be made without an existing ER or, at the very least, a membrane that contains the translocators required to import specific proteins into the ER (and lacks the translocators required to import the proteins that function in other organelles).

Thus it seems that the information required to construct a membrane-bounded organelle does not reside exclusively in the DNA that specifies the organelle's proteins. *Epigenetic* information in the form of at least one distinct protein that preexists in the organelle membrane is also required, and this information is passed from parent cell to progeny cell in the form of the organelle itself. Presumably, such information is essential for the propagation of the cell's compartmental organization, just as the information in DNA is essential for the propagation of its nucleotide and amino acid sequences.

Summary

Eucaryotic cells contain intracellular membranes that enclose nearly half the cell's total volume in separate intracellular compartments called organelles. The main types of membrane-bounded organelles that are present in all eucaryotic cells are the endoplasmic reticulum, Golgi apparatus, nucleus, mitochondria, lysosomes, endosomes, and peroxisomes; plant cells also contain plastids, such as chloroplasts. Each organelle contains a distinct set of proteins that mediates its unique functions.

Each newly synthesized organelle protein finds its way from the ribosome where it is made to the organelle where it functions by following a specific pathway, guided by signals in its amino acid sequence that function as signal peptides or signal patches. The signal peptides and patches are recognized by complementary receptor proteins in the target organelle. Proteins that function in the cytosol do not contain signal peptides or signal patches and therefore remain in the cytosol after they are synthesized.

Signal peptide cleavage of a type I membrane protein, HCMV US11, is dependent on its membrane anchor

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The human cytomegalovirus (HCMV) US11 polypeptide is a type I membrane glycoprotein that targets major histocompatibility complex (MHC) class I molecules for destruction in a proteasome-dependent manner. Although the US11 signal sequence appears to be a classical N-terminal signal peptide in terms of its sequence and cleavage site, a fraction of newly synthesized US11 molecules retain the signal peptide after the N-linked glycan has been attached and translation of the US11 polypeptide has been completed. Delayed cleavage of the US11 signal peptide is determined by the first four residues, the so-called n-region of the signal peptide. Its replacement with the four N-terminal residues of the H-2K^b signal sequence eliminates delayed cleavage. Surprisingly, a second region that affects the rate and extent of signal peptide cleavage is the transmembrane region close to the C-terminus of US11. Deletion of the transmembrane region of US11 (US11-180) significantly delays processing, a delay overcome by replacement with the H-2K^b signal sequence. Thus, elements at a considerable distance from the signal sequence affect its cleavage.
Keywords: ER subdomains/HCMV US11/post-translational ER processing/signal sequence cleavage/transmembrane anchor

Introduction

Membrane proteins and proteins destined for secretion are targeted to the appropriate intracellular membrane by their signal peptides (Martoglio and Dobberstein, 1998). In eukaryotes, signal peptides are 15–50 amino acids long and are usually located at the N-terminus (von Heijne, 1983). A typical signal peptide is comprised of three distinct regions: a polar N-terminal end (n-region) that may have a net positive charge, a central hydrophobic core (h-region) that consists of 6–15 hydrophobic amino acids, and a polar C-terminal (c-region) end that contains prolines and glycines (von Heijne, 1985). A signal peptide containing the consensus sequence and proper cleavage site ensures that proteins are inserted into the endoplasmic reticulum (ER) membrane and are processed properly.

Mutations within the sequence immediately downstream of the signal peptide affect protein processing, and can result in both inefficient and inaccurate cleavage (Russel and Model, 1981; Folz and Gordon, 1986; Andrews *et al.*, 1988; Wiren *et al.*, 1988). For example, replacement of glutamic acid for leucine at the +2 position of the phage coat protein cleavage site causes inefficient removal of its signal peptide (Russel and Model, 1981). When the propeptides of human pre-pro-apolipoprotein A-II and pre-pro-parathyroid hormone are deleted, five and six residues, respectively, the generation of an improper N-terminus and a failure to direct the nascent chain to the ER properly are observed (Folz and Gordon, 1986; Wiren *et al.*, 1988). Elements of the nascent chain at greater distances from the signal peptide are not known to affect signal peptide processing.

Shortly after its translation, the signal peptide interacts with signal recognition particle (SRP) and causes translational arrest (Walter and Blobel, 1981; Walter and Johnson, 1994). SRP is a ribonucleoprotein comprised of a 7S RNA associated with six different polypeptides (Walter and Blobel, 1980, 1982). The 54 kDa subunit of SRP interacts with the signal peptide through a hydrophobic region that promiscuously accommodates signal peptides of different lengths and sequences (Keenan *et al.*, 1998). The SRP–nascent polypeptide chain—ribosome complex is targeted to the ER membrane where SRP binds to the SRP receptor and the ribosome weakly interacts with the translocon (mainly comprised of the Sec61p complex) (Gorlich *et al.*, 1992; Kalies *et al.*, 1994; for reviews see Rapoport *et al.*, 1996; Hegde and Lingappa, 1999; Johnson and van Waes, 1999). The signal peptide is then transferred from the SRP into the channel of the translocon, where it directly associates with the Sec61α subunit of the Sec61 complex to promote tight interaction of the ribosome–nascent chain complex with the translocon (Jungnickel and Rapoport, 1995; Mothes *et al.*, 1998; Plath *et al.*, 1998). The signal peptide can also associate with the lipid bilayer and the TRAM protein (Martoglio *et al.*, 1995; Voigt *et al.*, 1996; Mothes *et al.*, 1997), which assists in protein transport through the translocon. The interaction of the signal peptide with the Sec61 complex may also induce the removal of a 'gating factor', possibly BiP, from the lumenal side of the translocon, to allow access of the nascent polypeptide to the ER lumen (Crowley *et al.*, 1994; Hamman *et al.*, 1998). Chain elongation is re-initiated, followed by signal peptide translocation through the Sec61 channel. The hydrophobic nature of the signal peptide allows its insertion into the ER membrane, followed by signal peptidase cleavage upon lumenal exposure of the cleavage site (Blobel and Dobberstein, 1975). This cleavage site is characterized by small uncharged residues at positions −1 and −3 (von Heijne, 1990). After signal peptide cleavage,

chain elongation of the nascent chain continues, while the signal peptide itself can be cleaved further by aminopeptidases or signal peptide peptidase (Lyko *et al.*, 1995; Martoglio *et al.*, 1997).

Signal peptidase is an endopeptidase that resembles other serine proteases (Dalbey and von Heijne, 1992) and performs a similar cleavage reaction for prokaryotic and eukaryotic signal peptidases. The crystal structure of the periplasmic domain of *Escherichia coli* leader peptidase (Paetzel *et al.*, 1998) reveals important mechanistic aspects of signal peptide cleavage: the catalytic site proposed to be close to the lipid bilayer is surrounded by a hydrophobic region, explaining the requirement for small uncharged, aliphatic residues at the −1 and −3 positions of the cleavage site (Paetzel *et al.*, 1998; von Heijne, 1998). The mammalian signal peptidase complex (SPC) is comprised of at least five subunits with molecular masses of 25, 23/22, 21, 18 and 12 kDa (Evans *et al.*, 1986). The non-catalytic subunits of the eukaryotic SPC may function as regulatory subunits for signal peptide recognition and are located in close proximity to the translocon (Meyer and Hartmann, 1997). The Sec61p complex interacts with the 25 kDa subunit of the SPC (SPC25), which suggests a tight interaction between the SPC and the Sec61 complex (Kalies *et al.*, 1998). This interaction may serve to recruit the SPC to the translocation site and thereby enhance the overall translocation efficiency of the nascent polypeptide.

The human cytomegalovirus (HCMV) gene products US11 and US2 target the major histocompatibility complex (MHC) class I molecules for destruction by the proteasome (Wiertz *et al.*, 1996a,b; Tortorella *et al.*, 1998). These viral proteins associate with the class I molecules in the ER and induce the dislocation of the class I heavy chains from the ER, probably via the Sec61p complex, for degradation in the cytosol (Wiertz *et al.*, 1996b). In all likelihood, a similar set of reactions is utilized for the removal and degradation of misfolded and abnormal ER proteins more generally (Bonifacino and Weissman, 1998). The HCMV US11 gene product is an ER-resident type I membrane glycoprotein (Figure 1), the single N-linked glycan attachment site of which is glycosylated quantitatively. The hydrophobic stretch at the N-terminus of US11 is characteristic of a signal peptide, while the hydrophobic stretch at the C-terminal end corresponds to a transmembrane/stop transfer sequence.

Here we report a highly unusual cleavage pattern for the US11 signal peptide. At least a fraction of the US11 signal peptide appears to be cleaved post-translationally. This trait is determined by the US11 signal peptide n-region. What cleavage occurs is also strongly influenced by the US11 transmembrane domain. Delayed cleavage of the US11 signal peptide may reflect the local ER environment in which dislocation takes place.

Results

The HCMV US11 signal peptide is cleaved post-translationally

HCMV US11 is a 215 residue ER-resident protein that targets MHC class I heavy chains for destruction by the proteasome. The detailed mechanism by which the viral
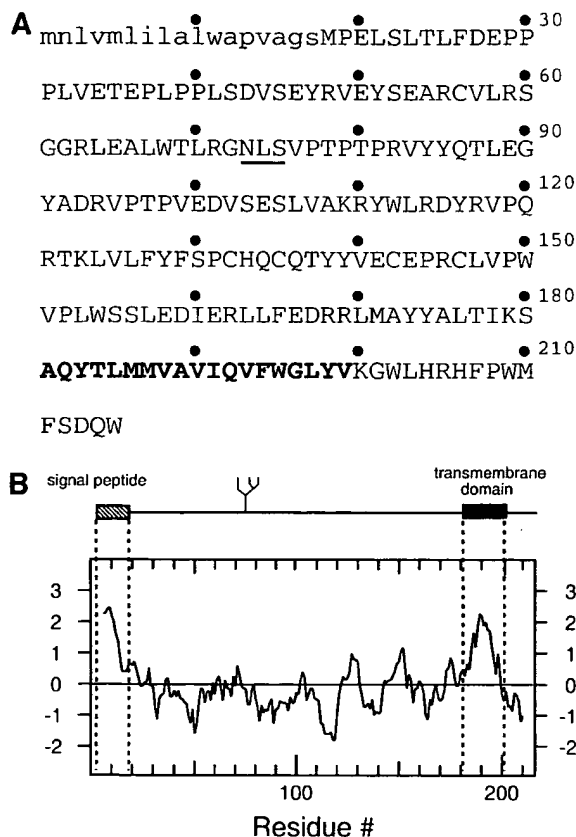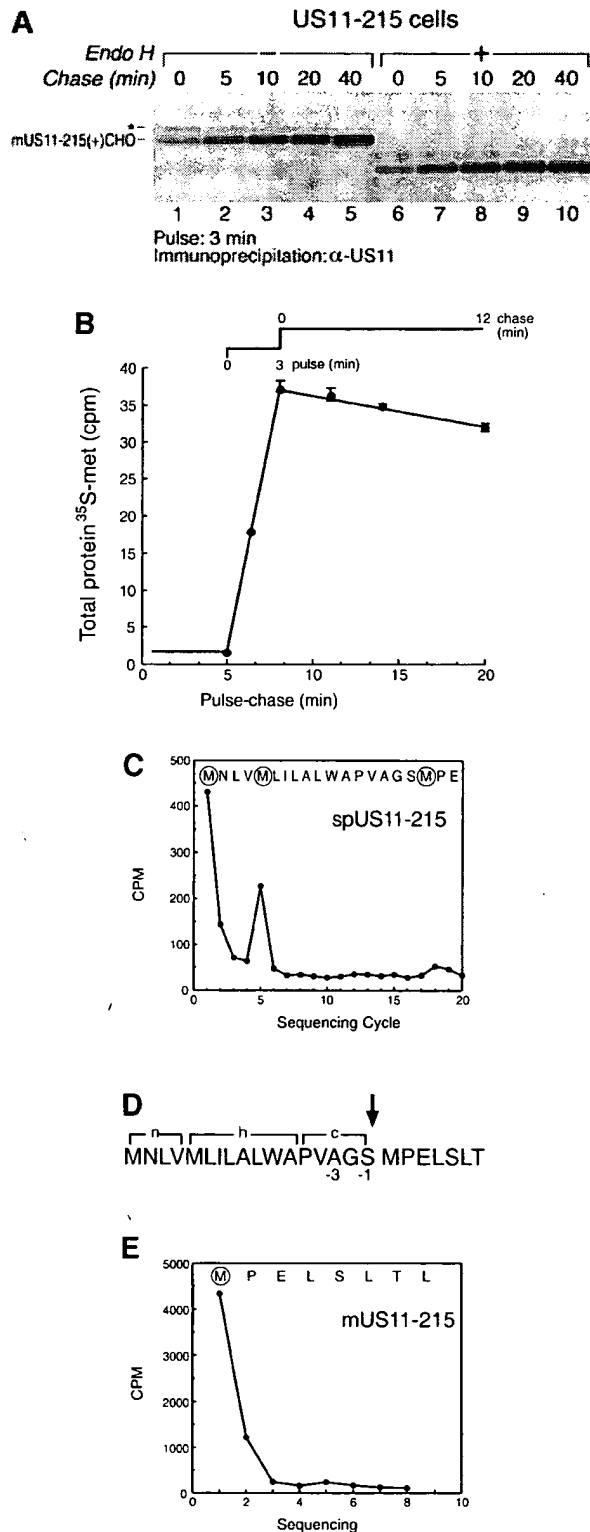
A
mnlvmlilalwapvagsMPELSLTLFDEPP ^{30}

PLVETEPLPPLSDVSEYRVEYSEARCVLRS ^{60}

GGRLEALWTLRGNLSVPTPTPRVYYQTLEG ^{90}

YADRVPTPVEDVSESLVAKRYWLRDYRVPQ ^{120}

RTKLVLFYFSPCHQCQTYYVECEPRCLVPW ^{150}

VPLWSSLEDIERLLFEDRRLMAYYALTIKS ^{180}

AQYTLMMVAVIQVFWGLYVKGWLHRHFPWM ^{210}

FSDQW

Fig. 1. (A) Amino acid sequence (single letter code) of HCMV US11. (B) Kyte–Doolittle hydropathy plot of US11. The predicted signal sequence is depicted in lower case. Bold face type represents the predicted transmembrane domain. The N-linked glycosylation site is underlined.

gene product accomplishes this is unclear, but is closely coupled to the biosynthesis of the class I and US11 products. We therefore examined whether the biosynthesis of US11 might reveal unique properties of the ER environment in which US11 normally functions. The maturation of US11 was examined in U373-MG cells stably transfected with US11 (US11-215 cells). US11-215 cells were metabolically labeled for 3 min with [^{35}S]methionine and chased for up to 40 min. The US11 protein was recovered from cell lysates by immunoprecipitation using a polyclonal anti-US11 serum (α-US11) and analyzed by SDS–PAGE (Figure 2A). Two species of US11 of distinct mobility were recovered at early time points (Figure 2B, lanes 1 and 2). The faster moving, major species is the ER-resident, mature form of US11 (mUS11-215). It has a mobility indistinguishable from that of US11 recovered from a microsome-supplemented cell-free translation system (D.Tortorella and H.L.Ploegh, unpublished data).

A precursor–product relationship between the two species was suggested by increased recovery at later chase points of mUS11-215 and decreased recovery of the slower moving species (*) (Figure 2A, lanes 1–4). The identity of the slower moving species (*) was unclear. Is it a distinct form of US11 or is it a protein associated with US11? Both mUS11-215 and the slower moving polypeptide (*) were recovered from SDS-denatured primary

immunoprecipitates in a second round of immunoprecipitation using α-US11 serum (D.Tortorella and H.L.Ploegh, unpublished data). We therefore conclude that the slowly migrating polypeptide is a distinct form of the US11 protein.

A   US11-215 cells

Endo H

Chase (min) 0 5 10 20 40   0 5 10 20 40

mUS11-215(+)CHO−

1 2 3 4 5 6 7 8 9 10

Pulse: 3 min
Immunoprecipitation: α-US11

B

0   12 chase (min)

0   3 pulse (min)

Total protein ^{35}S-met (cpm)

Pulse-chase (min)

C

(M)N L V(M)L I L A L W A P V A G S(M)P E

spUS11-215

CPM

Sequencing Cycle

D

MNLVMLILALWAPVAGS MPELSLT
-3 -1

E

(M) P E L S L T L

mUS11-215

CPM

Sequencing

The precursor–product conversion observed for the slower moving polypeptide (*) and mUS11-215 does not account fully for the amount of US11 recovered at early chase times. At the early time points of chase, there is a shortfall in the recovery of US11 (Figure 2A, lanes 1–3). This shortfall is not due to the continued incorporation of label during the chase (Figure 2B) and hence must result from the inability to retrieve all US11 at the early time points. Solubilization with the detergent SDS significantly improved recovery of both US11 polypeptides (* .and mUS11-215) at the early time points (D.Tortorella and H.L.Ploegh, unpublished data).

Earlier experiments failed to show the presence of endoglycosidase H (Endo H)-resistant US11 and indicated that US11 was confined to the ER, as confirmed by immunoelectron microscopy (Wiertz et al., 1996a). The primary structure of US11 predicts a single N-linked glycan (CHO) attachment site at position 73 (Asn73–Leu–Ser) (Figure 1). Both polypeptides (* and mUS11-215) recovered from the US11 immunoprecipitates were susceptible to digestion by Endo H (Figure 2A, lanes 6–10). The difference between these two molecules of US11 cannot be due to an unusual modification of the N-linked glycan and, therefore, must be caused by differences in the polypeptide backbone.

What type of modification could account for the presence of the slower moving species of US11? Based on the observed apparent molecular weight, the slowly migrating species of US11 may still contain the N-terminal signal peptide (spUS11-215). The polypeptide was isolated from [^{35}S]methionine-labeled cells and subjected to 20 cycles of Edman degradation (Figure 2C). The observed peaks of radioactivity fit the position of the methionines at the N-terminal end of the US11 precursor sequence. These results establish that, surprisingly, the slower moving form (*) (Figure 2A) is indeed a glycosylated US11 molecule that has retained its signal peptide.

The US11 signal peptide contains a typical cleavage site

The factor known to influence signal peptide cleavage is the presence of small amino acid side chains at the −1 and −3 position relative to the cleavage site. Does the US11 signal peptide cleavage site indeed contain the consensus

Fig. 2. Two forms of US11 exist early in biosynthesis. (A) US11-215 cells were pulsed for 3 min and chased for up to 40 min. Cells were lysed in 0.5% NP-40 and immunoprecipitated with anti-US11 serum (α-US11). The precipitates were analyzed by SDS–PAGE (12.5%). Two forms of US11 [* and mature US11-215 (+)CHO] were recovered from the US11-215 cell lysates (lanes 1–5). Half of the α-US11 precipitates were digested with Endo H (lanes 6–10). (B) Incorporation of [^{35}S]methionine was examined during a pulse–chase experiment of US11-215 cells. TCA-precipitable radioactivity (c.p.m.) from [^{35}S]methionine of each time point was plotted against the pulse–chase experiment. An average of three samples is represented at each value. (C) The slower moving US11 polypeptide (*) was subjected to N-terminal radiosequencing. The radioactivity (c.p.m.) from [^{35}S]methionine of each fraction of the N-terminal radiosequencing run was plotted against Edman cycle number. (D) The n-, h- and c-regions of the US11 signal peptide are shown. The site of signal peptide cleavage is indicated by an arrow. (E) N-terminal radiosequencing of the mature form of US11 (mUS11-215) plotted as radioactivity (c.p.m.) from [^{35}S]methionine versus Edman cycle number.

A

signal peptide | transmembrane region

US11-215 1 [   ] 215

US11-K^b$_{18-215}$ 1 [18   ] 215

K^b signal peptide

US11/A2$_{TM/CT}$ 1 [180   ]

HLA-A2 transmembrane/cytoplasmic tail

B

Cells: US11-215 | US11-K^b$_{18-215}$ | US11/A2$_{TM/CT}$

Chase (min): 0 4 8 16 | 0 4 8 16 | 0 4 8 16

spUS11-215
mUS11-215

mUS11/A2$_{TM/CT}$

1 2 3 4 5 6 7 8 9 10 11 12

Pulse: 3 min
Immunoprecipitation: αUS11

C

☒ spUS11-215 ■ mUS11-215

Total % 74 94 100 102

% recovery of US11: 18, 56, 82, 98, 102; 12, 2, 0

Chase (min)

☒ spUS11-K^b$_{18-215}$ ■ mUS11-K^b$_{18-215}$

Total % 92 102 100 100

% recovery of US11: 92, 102, 100, 100; 0, 0, 0, 0

Chase (min)

☒ spUS11/A2$_{TM/CT}$ ■ mUS11/A2$_{TM/CT}$

Total % 71 89 100 100

% recovery of US11: 71, 89, 100, 100; 0, 0, 0, 0
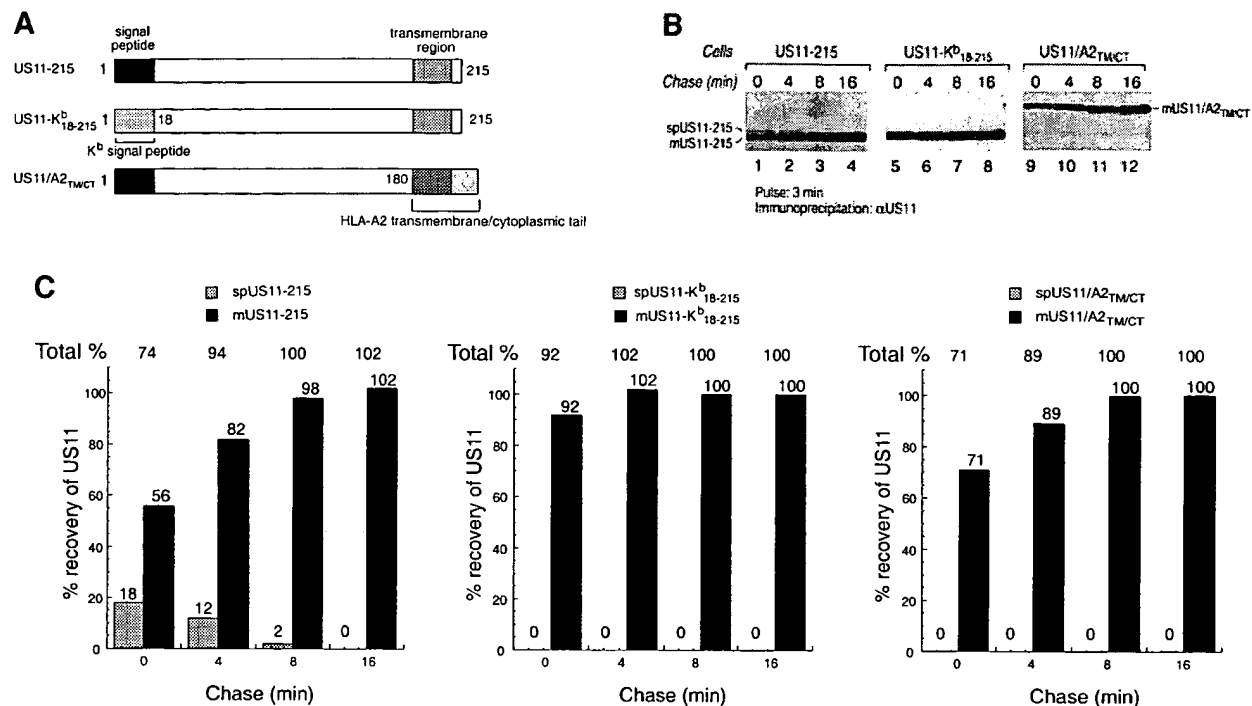
Chase (min)

Fig. 3. The delayed cleavage of the US11 signal peptide is determined by its signal sequence and transmembrane/cytoplasmic tail region. (A) The US11 chimeric molecules US11-K^b$_{18-215}$, US11/A2$_{TM/CT}$ and wild-type US11-215. (B) Processing of these molecules was examined in stable transfectants of MG-U373 cells using pulse–chase analysis. US11 was recovered from SDS lysates using α-US11 serum and analyzed by SDS–PAGE (12.5%). The signal peptide-containing form of US11 (spUS11-215) and the mature processed form of US11 (mUS11-215) are indicated. (C) The US11-215 molecules recovered from (B) were quantitated by a Molecular Dynamics Storm PhosphorImager. The US11 recovered at each time point is represented as percentage recovery of US11. The US11 recovered at the 8 min chase point was used as the 100% recovery value.

amino acids at the proper position? Analysis of the US11 primary sequence using the SignalP program (www.cbs.dtu.dk/services/SignalP/index.html) (Nielsen *et al.*, 1997a,b) predicts signal peptide cleavage of US11 to occur between residues 17 and 18 (Figure 2D). Serine (17) occurs at position –1 and alanine (15) at position –3, residues that are in perfect agreement with the consensus sequence for a signal peptide cleavage site. Methionine would be the N-terminus of the processed US11 molecule. Indeed, US11 isolated from [^{35}S]methionine-labeled US11-215 cells and subjected to eight cycles of N-terminal sequencing (Edman degradation) yielded methionine at position 1 (Figure 2E). Methionines within the N-terminal sequence of US11 occur at positions 5 and 18. Removal of only four residues from the N-terminus would not account for the mobility difference between the two forms of US11. Therefore, the methionine at position 18 must be the first residue of the mature US11 molecule. These results suggest that the unusual cleavage pattern of the US11 signal peptide is not due to an anomalous signal peptidase cleavage site.

The US11 signal peptide and the transmembrane region contribute to the delayed cleavage of the US11 signal s quence

N-terminal signal peptide cleavage is presumably determined solely by the sequence of the signal peptide itself (Martoglio and Dobberstein, 1998). Changes within the n-, h- or c-region of the signal peptide and the regions directly

downstream from the signal peptide affect signal peptide processing (Russel and Model, 1981; Folz and Gordon, 1986; Wiren *et al.*, 1988; Izard and Kendall, 1994). Can the US11 signal peptide itself or regions further downstream of the US11 signal sequence, such as the US11 transmembrane region, play a role in signal peptide cleavage? We generated US11-K^b$_{18-215}$ (Figure 3A), a chimeric molecule in which the US11 signal peptide was replaced with the signal peptide of the murine MHC class I heavy chain H-2K^b, a type I membrane protein. We also generated US11/A2$_{TM/CT}$ (Figure 3A), a chimeric molecule in which the transmembrane and cytoplasmic tail of US11 were replaced with the corresponding regions of human MHC class I heavy chain A2. Cleavage of the H-2K^b signal peptide should now generate the N-terminus of mature US11. Pulse–chase analysis of US11-215 cells shows the recovery of spUS11-215 and mUS11 at the early times points and a precursor–product relationship between the two polypeptides (Figure 3B, lanes 1–4, and C). For neither US11-K^b$_{18-215}$ nor US11/A2$_{TM/CT}$ did we observe the presence of a signal sequence-containing precursor (Figure 3B, lanes 5–8 and 9–12). This result suggests that unique features of US11's signal sequence and transmembrane domain contribute to the persistence of spUS11-215.

The recovery of mUS11-215 and US11/A2$_{TM/CT}$ increases with time (Figure 3B, lanes 1–4 and 9–12, and C). In contrast, recovery of US11-K^b$_{18-215}$ does not significantly change during the chase (Figure 3B, lanes 5–8, and C). We therefore conclude that the US11 signal
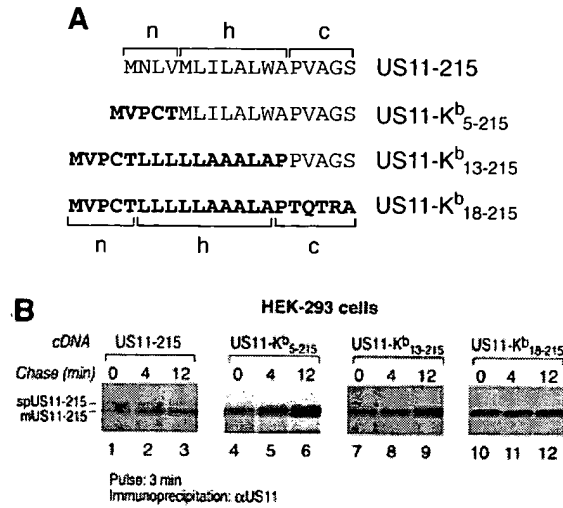
Fig. 4. The n-region of the US11-215 signal peptide is responsible for its delayed cleavage. (A) The amino acid sequences of the n-, h- and c-regions of US11-215, US11-K$^b_{5-215}$, US11-K$^b_{13-215}$ and US11-K$^b_{18-215}$. Bold letters represent the H-2K^b signal peptide. (B) US11-K$^b_{5-215}$ (lanes 4–6), US11-K$^b_{13-215}$ (lanes 7–9) and US11-K$^b_{18-215}$ (lanes 10–12) were transfected in HEK-293 cells and analyzed by pulse–chase analysis. US11 was recovered from SDS lysates using α-US11 serum and analyzed by SDS–PAGE (12.5%). The signal peptide-containing form of US11 (spUS11-215) and the mature processed form of US11 (mUS11-215) are indicated.
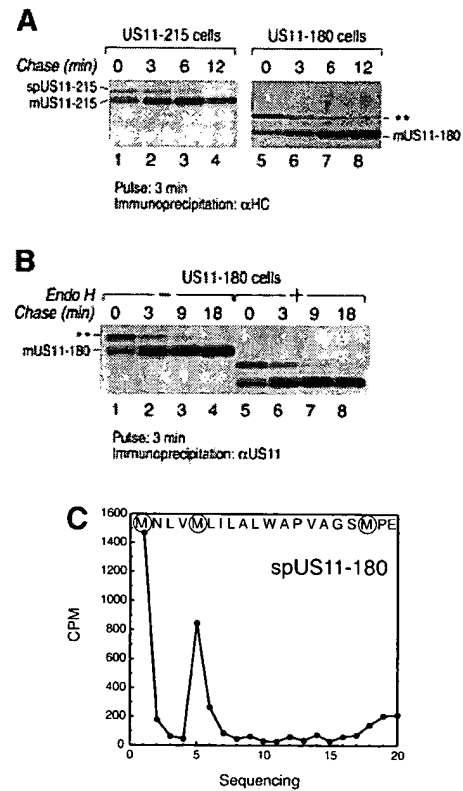

Fig. 5. Signal peptide cleavage of US11-180 is significantly delayed. (A) Processing of US11-215 and US11-180 was examined in stable transfectants of MG-U373 cells using pulse–chase analysis. US11 was recovered from SDS lysates using α-US11 serum and analyzed by SDS–PAGE (12.5%). The signal peptide-containing form of US11 (spUS11-215) and the mature processed form of US11 (mUS11-215) were immunoprecipitated from US11-215 cells (lanes 1–4). Two major species, ** and the mature processed form of US11-180 (mUS11-180), were recovered from US11-180 cells. (B) Half of the α-US11 precipitate recovered from a pulse–chase experiment of US11-180 cells was digested with Endo H (lanes 5–8). (C) The slower moving US11-180 polypeptide (**) was subjected to N-terminal radiosequencing. The radioactivity (c.p.m.) recovered at each Edman cycle is shown.

peptide is also responsible for the increased recovery of US11-215 and US11/A2$_{TM/CT}$ at the later time points. We suggest that the manner in which the US11 signal peptide initiates contact with the ER may contribute to its solubility properties.

The n-, h- and c-regions of the US11 signal peptide follow the proposed consensus for a cleavable N-terminal signal peptide. However, the results obtained for the chimeric US11-K$^b_{18-215}$ molecule suggest that the signal peptide itself may account for its delayed cleavage. To characterize further the segment of the US11 signal peptide that is responsible for delayed cleavage, we generated additional chimeras in which the n-region (US11-K$^b_{5-215}$) or n + h-regions (US11-K$^b_{13-215}$) of US11 are replaced with the corresponding regions of H-2K^b (Figure 4A). We transfected US11-215, US11-K$^b_{5-215}$, US11-K$^b_{13-215}$ and US11-K$^b_{18-215}$ into HEK-293 cells and examined their processing by pulse–chase analysis (Figure 4B). For US11-215, a signal peptide-containing form of US11 and the mature form of US11-215 were evident at early chase times (Figure 4B, lanes 1–3). The two polypeptides showed a precursor–product relationship. For the chimeras US11-K$^b_{5-215}$, US11-K$^b_{13-215}$ and US11-K$^b_{18-215}$, removal of the signal peptide is rapid and only the mature, cleaved form of US11 is recovered (Figure 4B, lanes 4–12). We conclude that features within the n-region of the US11 signal peptide contribute to its persistence.

During the chase, there is an increase in recovery of the mature form of US11-K$^b_{5-215}$ and US11-K$^b_{13-215}$ (Figure 4B, lanes 4–9), but not for US11-K$^b_{18-215}$ (Figures 4B, lanes 10–12, and 3B, lanes 5–8, and C). Therefore, the c-region of the US11 signal peptide

somehow contributes to recovery of mature US11. While the identity of the c-region does not affect the cleavage of the signal peptide, it does contribute to the recovery of mature US11. Perhaps the c-region is responsible for positioning nascent US11 relative to other components of the translocation machinery. This positioning may affect interactions of US11 with other ER components shortly after its completion, and hence its solubility. In contrast, the presence of the full K^b signal sequence neither delays signal peptide cleavage nor affects the recovery of US11 from cell lysates.

The US11 transmembrane region plays a role in US11 signal peptide cleavage

We next examined the role of the US11 transmembrane region in signal peptide cleavage. Such a role was suggested by the analysis of the US11/A2$_{TM/CT}$ chimeric construct (Figure 3). We generated a C-terminal truncation of US11 that lacks the predicted transmembrane segment and the cytoplasmic tail (US11-180) (Figure 1). The
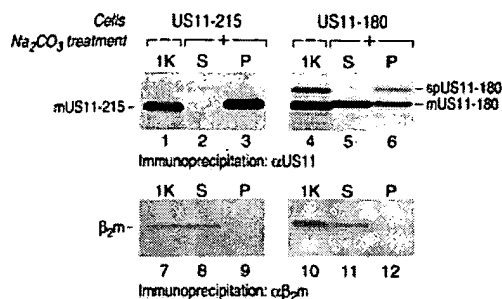
Fig. 6. US11-180 is a soluble molecule. US11-215 and US11-180 cells were metabolically labeled for 15 min. The cells were homogenized with glass beads and centrifuged at 1000 g. The 1000 g supernatant fractions were treated with 100 mM Na_2CO_3, followed by centrifugation at 150 000 g. US11 molecules (lanes 1–6) and β_2m (lanes 7–12) were recovered from the 1000 g (1K) pellet, 150 000 g supernatant (S) and the 150 000 g pellet (P) using α-US11 and α-β_2m serum. The immunoprecipitates were analyzed by SDS–PAGE (12.5%).
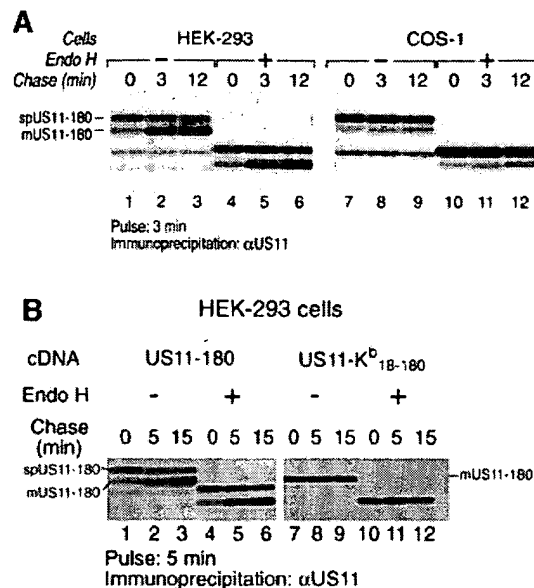

Fig. 7. The US11 signal peptide plays a major role in processing of US11-180. US11-180 cDNA was transfected into HEK-293 and COS-1 cells. (A) Processing of US11-180 was examined by pulse–chase analysis. US11-180 was recovered from SDS lysates using α-US11 serum and analyzed by SDS–PAGE (12.5%). Half of the immuno-precipitates recovered from the respective transfectants were treated with Endo H (lanes 4–6 and 10–12). (B) The US11 signal peptide chimeric molecule US11-K^{b}18-180 and US11-180 were transfected in HEK-293 cells and analyzed by pulse–chase analysis. US11 was recovered from SDS lysates using α-US11 serum and analyzed by SDS–PAGE (12.5%). Half of the immunoprecipitates recovered from the respective transfectants were treated with Endo H (lanes 4–6 and 10–12). The signal peptide-containing form of US11 (spUS11-180) and the mature processed form of US11 (mUS11-180) are indicated.

processing of wild-type US11-215 and US11-180 was examined in the appropriate U373-MG transfectants (Figure 5A). US11 recovered at the early chase times from US11-215 cells produced the usual pattern with respect to the precursor–product relationship of spUS11-215 and mUS11-215 (Figure 5A, lanes 1–4). Two major species were recovered from US11-180 cells (** and mUS11-180) (Figure 5A, lanes 5–8). A precursor–product relationship exists for the slower (**) and faster migrating species (mUS11-180) of US11-180. The two polypeptides recovered from the US11-180 transfectants represent distinct forms of the polypeptide backbone and both species of US11-180 are sensitive to Endo H (Figure 5B, compare lanes 1–4 and 5–8).

The slower moving species (**) was isolated from a US11-180 HEK-293 transfectant labeled with [35S]methionine and subjected to 20 cycles of Edman degradation (Figure 5C). The data showed persistence of the signal sequence. The absence of the transmembrane region of US11 thus strongly delays cleavage of its N-terminal signal peptide. An even more pronounced result was observed when US11-180 cDNA was transfected into HEK-293 and COS-1 cells (Figure 7).

mUS11-180 is a soluble protein

The Kyte–Doolittle hydropathy plot of US11 (Figure 1) suggests that the transmembrane region is located between residues 180 and 200. However, the hydrophobic nature of residues 180–200 does not ensure that it is in fact a transmembrane anchor. All attempts at proteolytic removal of the proposed cytoplasmic tail were without success. We performed Na_2CO_3 extractions to explore stable membrane insertion of US11-215 and US11-180 (Figure 6). US11-215 and US11-180 cells were labeled with [35S]methionine and broken with glass beads in the absence of detergent. Homogenates were then centrifuged at 1000 g to remove large debris, and the supernatant fraction was treated with 100 mM Na_2CO_3, followed by centrifugation at 150 000 g to sediment the extracted microsomes. US11-215 and US11-180 molecules were immunoprecipitated from detergent extracts prepared from the 1000 g pellet (Figure 6, lanes 1 and 4), the Na_2CO_3-treated 150 000 g soluble fraction (Figure 6,

lanes 2 and 5) and the 150 000 g pellet fraction (Figure 6, lanes 3 and 6). As a soluble, lumenal control protein, we used β_2-microglobulin (β_2m) (Figure 6, lanes 7–12). The US11-215 polypeptide is recovered exclusively from the 150 000 g pellet fraction (Figure 6, lane 3), whereas the bulk of β_2m is recovered from the 150 000 g soluble fraction (Figure 6, lane 8). These results confirm that US11-215 is a membrane protein. In contrast, the majority of US11-180 lacking its signal peptide (mUS11-180) and β_2m are recovered from the 150 000 g soluble fraction (Figure 6, lanes 5 and 11). These results confirm that mUS11-180 and β_2m are soluble, ER lumenal proteins.

A small fraction of mUS11-180 is recovered from the 150 000 g pellet fraction (Figure 6, lane 6) and may represent mUS11-180 that continues to associate with the ER membrane shortly after signal peptide cleavage and prior to its release into the ER lumen. Alternatively, a fraction of mUS11-180 may interact with an ER membrane protein in a Na_2CO_3-resistant manner. As might be expected, the signal peptide-containing form of US11-180 (spUS11-180) remains associated with the membrane fraction even after carbonate extraction (Figure 6, lane 6).

The identity of the signal sequence dictates delayed cleavage of the US11-180 molecule

For reasons of consistency with the data shown earlier, the experiments in Figure 5A were all conducted in U373-MG

cells stably transfected with the US11-180 cDNA. The delayed cleavage of the signal peptide of US11 is not an aberration of the recipient cell line used for transfection. In fact, when we used either HEK-293 or COS-1 cells in a transient transfection protocol, the persistence of the signal peptide-containing form of both US11-215 (Figure 4B, lanes 1–3) and US11-180 (Figure 7A) was much more pronounced. The relative amount of signal sequence-containing precursor of US11-180 was increased to the extreme, such that in COS-1 cells it is in fact the predominant form of US11-180 at the end of the chase (Figure 7A, lanes 7–12). Our data show that the anomalous behavior of the US11 signal peptide is intrinsic to the US11 molecule. In transfection experiments exploiting COS-1 cells to express other type I membrane proteins, the persistence of signal peptides was not observed (Huppa and Ploegh, 1997) and to our knowledge has not been reported by others.

We next addressed the contribution of the signal sequence's identity to the delayed cleavage observed for US11-180. We generated a chimeric molecule, US11-K^b$_{18-180}$, in which the US11-180 signal peptide is replaced with the H-2K^b signal peptide (Figure 3A). We transfected US11-180 and US11-K^b$_{18-180}$ into HEK-293 cells and examined their processing by pulse–chase analysis (Figure 7B). The immunoprecipitates were treated with Endo H to verify glycosylation and ER insertion (Figure 7B, lanes 4–6 and 10–12). For US11-180 carrying the US11 signal peptide, the signal peptide-containing form of spUS11-180 and the mature processed form of US11-180 were observed throughout the chase (Figure 7B, lanes 1–3). In contrast, a single polypeptide with a mobility similar to that of mUS11-180 is recovered from US11-K^b$_{18-180}$ transfectants (Figure 7B, lanes 7–9). Delayed cleavage of the US11-180 signal peptide no longer occurs when the US11 signal peptide is replaced with the H-2K^b signal peptide. Not only the US11 transmembrane segment, but also features of the US11 signal sequence itself play a major role in US11 signal peptide cleavage.

Discussion

We describe here the unusual properties of the signal sequence of HCMV US11, a type I membrane glycoprotein. Elements contained within the signal sequence's N-terminal segment (Met–Asn–Leu–Val) are responsible for delayed cleavage, such that a fully glycosylated, signal peptide-bearing intermediate is readily detected. In addition, the C-terminal membrane anchor also affects the rate of signal peptide cleavage; a US11 variant lacking its transmembrane/cytoplasmic tail segment (US11-180) shows an even greater delay in signal peptide cleavage than is seen for full-length US11. This effect is at its most extreme in COS-1 cells, where the glycosylated, signal peptide-containing US11-180 protein (spUS11-180) is the majority of US11 polypeptide that persists. To account for these findings, we propose an extended interaction of the signal peptide and transmembrane segment with the processing apparatus.

Conformity with the consensus parameters within the n-, h- and c-regions of the signal peptide predicts proper cleavage of an N-terminal signal peptide. The US11 signal

peptide sequence fits the consensus parameters within the n-, h- and c-regions, yet fails to be cleaved efficiently from the nascent chain. Chimeric molecules in which regions (n, n + h or n + h + c) of the US11 signal peptide were replaced with the corresponding regions of the murine class I heavy chain H-2K^b signal peptide demonstrate that it is the n-region of the US11 signal sequence that is mostly responsible for the delayed cleavage of the US11 signal peptide (Figure 4). An irregular n-region has been observed to affect signal peptide processing; a surfeit of positive charges within the n-region of the HIV-1 gp-120 signal sequence probably accounts for its inefficient cleavage (Li et al., 1994, 1996). This aberrant form of gp-120 does not exit the ER and, therefore, cannot be incorporated into a nascent virion. We note that the persistence of the uncleaved signal sequence on gp-120 was never directly shown by sequence analysis.

Regions outside the signal peptide can also influence its cleavage. In pre-pro-apolipoprotein A-II and pre-pro-parathyroid hormone, removal of the propeptide that is immediately downstream of the signal peptide influenced ER protein translocation and proper signal peptide processing (Russel and Model, 1981; Folz and Gordon, 1986; Andrews et al., 1988; Wiren et al., 1988). These changes mostly affect the site of cleavage, shifting it a few residues downstream, while their effect on the rate of signal peptide cleavage was not addressed in any detail. In addition, a mutation at the +2 position of the signal peptide cleavage site of phage coat protein also results in inefficient cleavage (Russel and Model, 1981). All of these mutations are localized immediately downstream of the signal peptide. In contradistinction to such signal sequence-proximal alterations, the transmembrane anchor of US11, at a considerable distance (~160 residues) from the US11 signal sequence, strongly influences signal sequence cleavage. The rate of signal peptide cleavage for the US11 molecule lacking its transmembrane/cytoplasmic tail region (US11-180) is significantly delayed when compared with that seen for wild-type US11 (Figure 5). Replacement of the US11 signal sequence for that of H-2K^b results in rapid processing of US11 lacking the transmembrane segment, such that signal sequence-containing forms are no longer detected. The unprocessed US11-180 polypeptide is probably in an orientation unfavorable for signal peptide cleavage, and the presence of the US11 transmembrane anchor is clearly required for efficient signal peptide processing (Figure 8).

How can the US11 transmembrane anchor accelerate removal of the US11 signal peptide? The transmembrane domain may interact with the signal peptide and position the signal peptide to facilitate access to the cleavage site. Alternatively, the transmembrane anchor may interact with the SPC and enhance recognition of the US11 signal peptide for reasons of physical proximity. While the specificity of signal peptide cleavage is appreciated in terms of the minimum sequence requirements, cleavage itself is a highly regulated process, the dynamics of which are not well understood. The non-catalytic subunits of the SPC have been cloned and isolated, yet their function remains to be determined. Our results show that regulation of signal peptide cleavage may involve cis-acting elements within the polypeptide that act at considerable distance
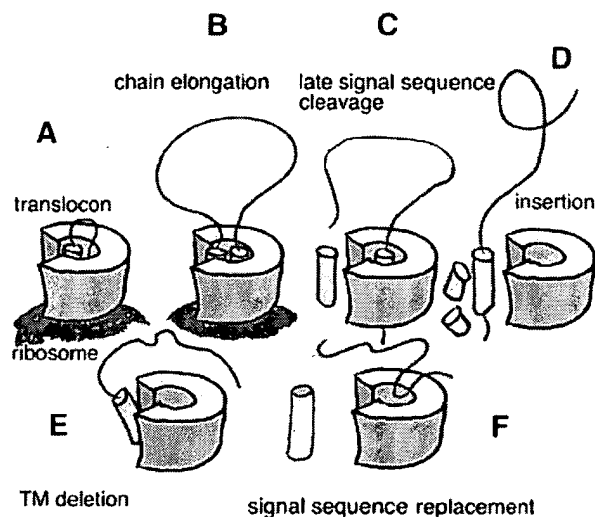
Fig. 8. Model of HCMV US11 signal peptide cleavage. (A) The signal peptide (pink) is inserted into the translocon, followed by (B) chain elongation of the US11 nascent polypeptide. (C) Upon completion of US11 translation, the US11 transmembrane segment (blue) may interact with the signal peptide to delay signal peptide cleavage. (D) Upon cleavage of the signal peptide, the US11 molecule inserts into the lipid bilayer; the signal peptide itself may be cleaved further by signal peptide peptidase. (E) The signal peptide of a truncated US11 molecule that lacks its transmembrane region and cytoplasmic tail (US11-180) is cleaved inefficiently from the nascent polypeptide. (F) Replacement of the US11 signal peptide in US11-180 with the H-2K^b signal peptide (green) results in efficient processing. The US11 transmembrane domain may position the signal peptide in an orientation favorable for cleavage.

from the actual cleavage site. Such elements could perhaps interact with the non-catalytic subunits of signal peptidase.

Immunoelectron microscopy, the maturation status of its single N-linked glycan and the kinetics with which it catalyzes accelerated destruction of class I molecules all place US11 in the ER. The ER environment of the US11 signal peptide may help determine the unusual signal peptide cleavage pattern that we observe. The site of signal peptide cleavage is in the ER and is postulated to be in close proximity to the translocon (Kalies *et al.*, 1998). An intrinsic feature of the US11 signal peptide, more specifically the c-region of the signal peptide, may dictate an association with complexes within the ER as judged from the observed cleavage in detergent extractability (Figure 4 and D.Tortorella and H.L.Ploegh, unpublished data). Shortly after signal peptide cleavage, the recovery of the processed form of US11 increases over the chase period. We suggest that these early biosynthetic forms of US11 may reside in specialized regions of the ER.

To address an issue more peripheral to the central claims of this study: is the cleavage pattern of US11's signal sequence related to US11-induced class I degradation? The signal peptide of the chimeric molecule US11–K$^b_{18-215}$ is cleaved rapidly and this molecule readily supports class I destruction (D.Tortorella and H.L.Ploegh, unpublished data). Therefore, the identity of the US11 signal peptide itself is not essential for the ability of US11 to accelerate class I degradation. The signal peptide of the chimera US11/A2$_{TM/CT}$ is also cleaved rapidly, but class I heavy chains are not degraded in

US11/A2$_{TM/CT}$-expressing cells (D.Tortorella and H.L.Ploegh, unpublished data). Deletion of US11's cytoplasmic tail does not abolish degradation of class I heavy chains (D.Tortorella and H.L.Ploegh, unpublished data), and consequently the identity of the transmembrane segment of US11 should be considered essential to its function.

If our interpretation is correct, then perhaps the interaction of the US11 signal peptide and US11 transmembrane segment would help keep the Sec61 complex and its accessories in a configuration that allows recruitment of the class I heavy chains to the translocon. The recorded efficiency of US11-mediated dislocation suggests that the process is tightly linked, temporally and perhaps physically, to protein translocation into the ER. Thus, close proximity of US11 to the translocation apparatus and efficient gating of the protein channel might account for the speed of the dislocation reaction. Ultimately, this aspect must be related to the properties of US11 itself. The unusual maturation of US11, as described here, may turn out be an important aspect of how the dislocation apparatus is put in place.

Materials and methods

Cell lines and antibody

U373-MG astrocytoma cells transfected with the US11-215 cDNA were prepared as described (Jones *et al.*, 1995; Kim *et al.*, 1995) and cells were maintained in Dulbecco's modified Eagle's medium (DMEM) supplemented with 5% fetal calf serum (FCS) and 5% calf serum. US11-201, US11-180, US11K$^b_{18-215}$ and US11/A2 cells were maintained in DMEM supplemented with 5% FCS, 5% calf serum and 0.5 mg/ml geneticin (Gibco, Fredrick, MD). The human embryonic kidney cell line (HEK-293) was maintained in DMEM supplemented with 5% FCS and 5% calf serum. The anti-US11 serum was generated by immunizing rabbits with fragments of US11 (amino acids 18–36, 104–122 and 194–210) conjugated to keyhole limpet hemocyanin (Story *et al.*, 1999). The anti-class I heavy chain serum was generated by immunizing rabbits with the bacterially expressed lumenal fragment of HLA-A2 and HLA-B27 heavy chains (Tortorella *et al.*, 1998). The anti-β$_2$m serum was generated by immunizing rabbits with bacterially expressed human β$_2$m.

Metabolic labeling of cells and pulse–chase analysis

Cells were detached by trypsin treatment, followed by starvation in methionine/cysteine-free DMEM for 45 min at 37°C. Cells were metabolically labeled with 500 µCi of [^{35}S]methionine/cysteine (1200 Ci/mmol; NEN-Dupont, Boston, MA)/ml at 37°C for the times indicated. In pulse–chase experiments, cells were radiolabeled as above and were chased for the times indicated in DMEM containing non-radiolabeled methionine (2.5 mM) and cysteine (0.5 mM). Cells were then lysed in NP-40 lysis buffer (10 mM Tris pH 7.8, 150 mM NaCl, 5 mM MgCl$_2$, 0.5% NP-40) supplemented with 1.5 µg/ml aprotinin, 1 µM leupeptin, 2 mM phenylmethylsulfonyl fluoride (PMSF) followed by immunoprecipitation (see below). For cells lysed in 1% SDS, the SDS concentration was adjusted, prior to immunoprecipitation, to 0.063% with the NP-40 lysis mix.

Immunoprecipitation

Following cell lysis, cell debris was removed by centrifugation at 10 000 *g* for 10 min. Non-specific binding proteins were removed from the cell lysates by the addition of 3 µl/ml normal rabbit serum, 3 µl/ml normal mouse serum and formalin-fixed, heat-killed *Staphylococcus aureus* for 1 h at 4°C. Immunoprecipitation was performed by incubation with antiserum for 45 min at 4°C, followed by the addition of *S.aureus* for 45 min at 4°C. The pelleted *S.aureus* were washed four times with washing buffer (0.5% NP-40 in 50 mM Tris pH 7.4, 150 mM NaCl and 5 mM EDTA). The pellet was resuspended in SDS sample buffer (4% SDS, 5% β-mercaptoethanol, 10% glycerol, 0.025% bromophenol blue in 62.5 mM Tris pH 6.8) and the released materials were subjected to 12.5% SDS–PAGE.

cDNA, transfection and Endo H digestion

The cDNA of full-length US11 was cloned from the AD169 HCMV genome using the following primers: 5' primer, CCGCTCCGAGCG-GCGTCGACACCACCATGGAACCTTGTAATGCTTATTCTAGC; 3' primer, GCTCTAGAGCTCACCACTGGTCCGAAAACATCCAG. The US11 cDNA was cloned into the eukaryotic expression vector pcDNA 3.1 (Invitrogen, Carlsbad, CA) using the *Xho–Xba* restriction site in its polylinker region. US11-180 was subcloned from US11 (pcDNA3.1). The chimeric molecules: US11/A2$_{TM/CT}$ [US11(amino acids 1–178)/HLA-A2(amino acids 307–365)]; US11-K$^b_{5-215}$ [H-2K^b(amino acids 1–5)/US11(amino acids 5–215)]; US11-K$^b_{13-215}$ [H-2K^b(amino acids 1–16)/US11(amino acids 13–215)]; US11-K$^b_{18-215}$ [H-2K^b(amino acids 1–21)/US11(amino acids 18–215)]; and US11-K$^b_{18-180}$ [H-2K^b(amino acids 1–21)/US11(amino acids 18–180)] were generated by initially cloning the desired fragment followed by ligation of two of the respective fragments. Using primers specific to the ends of the ligated molecule, it was recloned and inserted into pcDNA3.1. A liposome-mediated transfection (Lipofectamine, Gibco, Fredrick, MD) protocol was performed as described by the manufacturer (4 µg of DNA/20 µl of lipofectamine/ 10 cm dish of cells). Endo H (New England Biolabs) digestion was performed as described by the manufacturer.

Gel electrophoresis

SDS–PAGE and fluorography were performed as described (Ploegh, 1995). For N-terminal sequencing, the immunoprecipitated US11 protein was resolved by SDS–PAGE and transferred to a PVDF membrane (0.22 µm pore size) in transfer buffer (48 mM Tris-base, 39 mM glycine, 0.037% SDS, 20% methanol) using a semi-dry blotting apparatus (Buchler Instruments, Kansas, MO).

N-terminal sequence analysis

The PVDF membrane that contained the polypeptide of interest was subjected to automated Edman degradation using an Applied Biosystem Protein Sequencer, Model 477, using ATZ chemistry, at the Biopolymers Laboratory at MIT, Center for Cancer Research. The fractions from each degradation sequencing cycle were collected and counted by liquid scintillation spectrometry.

Na$_2$CO$_3$ treatment

US11-215 and US11-180 cells were metabolically labeled for 15 min and then washed twice in 50 mM Tris pH 7.5, 250 mM sucrose (homogenization buffer). The cells were resuspended in homogenization buffer and broken by vortexing in the presence of 106 µm glass beads. The homogenate was centrifuged at 1000 *g* for 5 min; the pellet fraction was resuspended in NP-40 lysis mix (see above) and the supernatant was treated with Na$_2$CO$_3$ (100 mM final) for 30 min at 4°C (Fujiki *et al.*, 1982). The Na$_2$CO$_3$-treated samples were centrifuged at 150 000 *g* using a TLA 100.2 rotor in a Beckman centrifuge. The 150 000 *g* high pH supernatant was adjusted to pH 7 with 1 M HCl and diluted to a final 1× NP-40 lysis mix. The 150 000 *g* pellet was washed twice with homogenization buffer and then resuspended in 1× NP-40 lysis mix. US11 and β$_2$m were immunoprecipitated from the 1000 *g* pellet, 150 000 *g* supernatant and the 150 000 *g* pellet with the respective antibody.

Acknowledgements

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Ashkenazi et al.
App. No.	:	09/903,925
Filed	:	July 11, 2001
For	:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
Examiner	:	Hamud, Fozia M

Group Art Unit 1647

CERTIFICATE OF EXPRESS MAILING

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DECLARATION OF AVI ASHKENAZI, Ph.D UNDER 37 C.F.R. § 1.132

I, Avi Ashkenazi, Ph.D. declare and say as follows: -

1.   I am Director and Staff Scientist at the Molecular Oncology Department of Genentech, Inc., South San Francisco, CA 94080.

2.   I joined Genentech in 1988 as a postdoctoral fellow. Since then, I have investigated a variety of cellular signal transduction mechanisms, including apoptosis, and have developed technologies to modulate such mechanisms as a means of therapeutic intervention in cancer and autoimmune disease. I am currently involved in the investigation of a series of secreted proteins over-expressed in tumors, with the aim to identify useful targets for the development of therapeutic antibodies for cancer treatment.

3.   My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).

4.   Gene amplification is a process in which chromosomes undergo changes to contain multiple copies of certain genes that normally exist as a single copy, and is an important factor in the pathophysiology of cancer. Amplification of certain genes (e.g., Myc or Her2/Neu)

gives cancer cells a growth or survival advantage relative to normal cells, and might also provide a mechanism of tumor cell resistance to chemotherapy or radiotherapy.

5.   If gene amplification results in over-expression of the mRNA and the corresponding gene product, then it identifies that gene product as a promising target for cancer therapy, for example by the therapeutic antibody approach. Even in the absence of over-expression of the gene product, amplification of a cancer marker gene - as detected, for example, by the reverse transcriptase TaqMan® PCR or the fluorescence *in situ* hybridization (FISH) assays -is useful in the diagnosis or classification of cancer, or in predicting or monitoring the efficacy of cancer therapy. An increase in gene copy number can result not only from intrachromosomal changes but also from chromosomal aneuploidy. It is important to understand that detection of gene amplification can be used for cancer diagnosis even if the determination includes measurement of chromosomal aneuploidy. Indeed, as long as a significant difference relative to normal tissue is detected, it is irrelevant if the signal originates from an increase in the number of gene copies per chromosome and/or an abnormal number of chromosomes.

6.   I understand that according to the Patent Office, absent data demonstrating that the increased copy number of a gene in certain types of cancer leads to increased expression of its product, gene amplification data are insufficient to provide substantial utility or well established utility for the gene product (the encoded polypeptide), or an antibody specifically binding the encoded polypeptide. However, even when amplification of a cancer marker gene does not result in significant over-expression of the corresponding gene product, this very absence of gene product over-expression still provides significant information for cancer diagnosis and treatment. Thus, if over-expression of the gene product does not parallel gene amplification in certain tumor types but does so in others, then parallel monitoring of gene amplification and gene product over-expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over-expression is crucial information for the practicing clinician. If a gene is amplified but the corresponding gene product is not over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

7.   I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that wilful false statements and the like so

made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the
United States Code and that such willful statements may jeopardize the validity of the
application or any patent issued thereon.

By: _Avi Ashkenazi_   Date: _9/15/03_

Avi Ashkenazi, Ph.D.

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CURRICULUM VITAE
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July 2003

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Education:

1983:	B.S. in Biochemistry, with honors, Hebrew University, Israel
1986:	Ph.D. in Biochemistry, Hebrew University, Israel

Employment:

1983-1986:	Teaching assistant, undergraduate level course in Biochemistry
1985-1986:	Teaching assistant, graduate level course on Signal Transduction
1986 - 1988:	Postdoctoral fellow, Hormone Research Dept., UCSF, and Developmental Biology Dept., Genentech, Inc., with J. Ramachandran
1988 - 1989:	Postdoctoral fellow, Molecular Biology Dept., Genentech, Inc., with D. Capon
1989 - 1993:	Scientist, Molecular Biology Dept., Genentech, Inc.
1994 -1996:	Senior Scientist, Molecular Oncology Dept., Genentech, Inc.
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1997-1990:	Senior Scientist and preclinical project team leader, Genentech, Inc.
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Awards:

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Editorial:

Editorial Board Member: Current Biology

Associate Editor, Clinical Cancer Research.

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Refereed papers:

1. Gertler, A., Ashkenazi, A., and Madar, Z. Binding sites for human growth hormone and ovine and bovine prolactins in the mammary gland and liver of the lactating cow. *Mol. Cell. Endocrinol.* 34, 51-57 (1984).

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